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Best Local Similarity 99.8%;
Matches 833; Conservative (
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CORGANISM: Homo sapiens
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               US-09-439-313-531
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FNCTH: 879
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Fatent No. 6329505
FABREAL INFORMATION:
APPLICANT: Nu. JiangChun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Read, Michael
APPLICANT: Read, Steven G.
APPLICANT: Ranger, Mark
APPLICANT: Ranger, Mark
APPLICANT: Rougel
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APPLICANT: Rougel
APPLICANT: Oby, Canig
TITLE OF INVENTION: DAY, Craig
TITLE OF INVENTION: DAY, CANIG
FILE REFERENCE: 210121.4279
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEG ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
FURNATION: OF 511
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Pred. No. 4.4e-238;
0; Mismatches 2;
US-09-062-451-295
US-09-352-G16A-369
US-09-636-215-369
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US-09-636-215-531

Sequence 531, Application US/09636215

Patent No. 6620925

GENERAL INFORMATION:
APPLICANT: Nithon, Davin C.
APPLICANT: Mitchan, Janinfer L.
APPLICANT: Mitchan, Janinfer L.
APPLICANT: Mitchan, Dannifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, Thomas S.
APPLICANT: Garter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Wasir A.W.
APPLICANT: Skeiky, Wasir A.W.
APPLICANT: Stolk, Jahiun
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APPLICANT: Ske
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ORGANISM: Homo sapiens
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                                                                           GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAAAGCTGCCTGGTGGGGGTAAAGT
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Length
                 Indels
Query Match

89.2%; Score 831.8; DB 4;
Best Local Similarity 99.8%; Pred. No. 4.4e-238;
Matches 833; Conservative 0; Mismatches 2;
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APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT APPLICATION NUMBER: Ug/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 531
BENGTH: 879 Score 831.8; DB 4; Pred. No. 4.4e-238; 0; Mismatches 2; Query Match
Best Local Similarity 99.8%;
Matches 833; Conservative TYPE: DNA CRGANISM: Homo sapiens US-09-685-166A-531 639 522 669 42 159 579 159 102 279 gg Š g ŏ 음 상 음 6 B 6 g 8 8 86868686

ö 518 878 821 101 278 281 398 341 458 401 461 578 521 102 GACGCTTGGGAGCAAGAGGGGCGCAGTGCCACTGCTTCCCCTGCTGCAGGGGGGG 161 221 761 219 CGGCAAGAGCAACGTGGGGCCTTGGGGAACTAACGATGACGCCCTTCATGGATCCCAGGCGC CTTCATGGATCCCAGGCGCCTTCATGGGTGCGTTGGGGAACCTACGATGACAGCGCCTTCATGATCCCAG GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCCACTGATCC 42 CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA 222 GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT 99 chadadadadadahadadanadaradaradahadahadahadahadahadaha GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGGTAAAGT 159 GACGCTTGGGAGCAAGAGTGCTGCTGCTGCCTTCCCCTGCTGCTGCAGGGGGAAG Gaps 933 876 TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG RESULT 4

US-09-429-755-314

US-09-429-755-314

Sequence 314, Application US/09429755A

Patent No. 6656480

GENERAL INFORMATION:

APPLICANT: Fridadis, Tony N.

APPLICANT: Fridadis, Tony N.

APPLICANT: Reed, Steven G.

APPLICANT: Misher, Lynda

TILE OF INVENTION: ORNERS WATER

TILE OF INVENTION: TOWEST NO.

TILE REPERENCE: 210121.419C6

CURRENT APPLICATION NUMBER: US906

CURRENT FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 315

SEQ ID NO 314 ô Length 879; Indels Query Match

89.2%; Score 831.8; DB 4;
Best Local Similarity 99.8%; Pred. No. 4.4e-238;
Matches 833; Conservative 0; Mismatches 2; TYPE: DNA
CORGANISM: Homo sapiens
US-09-429-755-314 759 8 6 8 6

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Sequence 530, Application US/09439313

Sequence 530, Application US/09439313

SEREAL INFORMATION:

APPLICANT: No. 6329505

APPLICANT: Mingerhum Control Control Candifor Ca
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89.2%; Score 831.8; DB 4;
Best Local Similarity 99.8%; Pred. No. 6.7e-238;
Matches 833; Conservative 0; Mismatches 2;
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CORGANISM: Homo sapiens
US-09-439-313-530
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Harlocker, Susan L.

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                                                   Score 831.8; DB 4;
Pred. No. 6.7e-238;
0; Mismatches 2;
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Best Local Similarity 99.8%;
Matches 833; Conservative
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                   Sequence 530, Application US/09685166A Patent No. 6630305 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L.
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89.2%; Score 831.8; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 6.7e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0;
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REFERENCE: 21011.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEC ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 530
LENGTH: 1852
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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; ORGANISM: Homo sapiens
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Db 1191 GGCCGTACAATGCCAGGAAGATG	OY 579 AAATATTCCAGATGAGTATGGAAATA(Oy 639 ATTAATGGCCAAAGCACTGCTCTTATI	Oy 699 CCTCACACCACTACTACTACTACTACTACTACTACTACTA	Oy 759 CAAGAAAAAGGGAATTTAAATGGGC 	Oy 819 IGTATGTTGTGGATCAGCAAGTATAG 	Qy 879 ITCTCAAGATCTGGAAAGACGGCCAG.	RESULT 9 789A-291/c US-08-991-789A-291/c ; Sequence 291, Application US/08991789A ; Patent No. 6225054 ; GENERAL INFORMATION: ; APPLICANT: Frudakis, Tony N.	Smith, John M. Reed, Steven G. TITLE OF INVENTION TONEDSITION MINIST OF SECTION S. COMPOSITION IN STREETMENT ALL MINISTED OF SECTION S. 202	CORRESPONDENCE 392 CORRESPONDENCE 392 ADDRESSEE: Seed IP Law Gro STREET: 701 Fifth Avenue, 3 CITY: Seattle	STATE: WESTINGTON COUNTRY: USA ZIP: 98104-7092 COMPUTER READABLE FORM:	MEDLUM TYPE: Floppy disk MEDLUM TYPE: Floppy disk MONDUTE: SCOMPATING SYSTEM: PC-DOS/M SOFTWARE: Patentin Release	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/; FILING DATE: 11-Dec-1997 CLASSIFICATION: <unknowt></unknowt>	ATTORNEY AGENT INFORMATION: NAME: POTTER, Jane E. R. REGISTRATION NUMBER: 33,333 REFERENCE/DOCKET NUMBER: 2.	TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 291:	SEQUENCE CHARACTERISTICS: ; TABLE MUCHEL SAITS ; TYPE: MUCHELC ACID ; TREANDEDNESS: SINGLE	SEQUENCE DESCRIPTION: SEQ ID NO. US-08-991-789A-291	Query Match 87.9%; Score 8 Best Local Similarity 99.6%; Pred. h Matches 832; Conservative 0; Mism
Db 1371 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTAAT 1430	OY 759 CAAGAAAAAGGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818 Db 1431 CAAGAAAAAGGGAATTTAAATGCGCTGGATAGATATGGAAGAAGACTCCTCATACTTGC 1490	Qy 819 TGTAIGTIGGAICACGAAGTAIAGICAGCCCTCTACTIGAGCAAAAIGTIGAIGTAIC 878 Db 1491 TGTAIGTIGGAICAGCAAAGTAIAGTCAGCCTCTACTIGAGCAAAAIGTIGAIGTAIC 1550	Qy 879 TICTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTGATCATCATCTG 933	RESULT 8 12-09-429-755-313 Semience 313 andication HC/Nodobres	; Patent No. 6656480 ; GENERAL INFORMATION: ; APPLICANT: Frudakis, Tony N.	APPLICANT: Reed, Steven G. APPLICANT: Misher, Lynda APPLICANT: Misher, Lynda APPLICANT: Patter, Marc W. APPLICANT: PATTER APPLICANT: PATTE	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER TITLE REFERENCE: 210121,419CG; CURRENT APPLICATION NUMBER: US/09/429,755A; CURRENT FILING DATE: 1999-10-28; NUMBER OF SEQ ID NOS: 315; SOFTWARE: FastSEQ for Windows Version 3.0	; SEQ ID NO 313 ; LENGTH: 1852 ; TYPE: DNA ; ORGANIEM: Homo sapiens	Query Match 89.2%; Score 831.8; DB 4; Length 1852; Best Local Similarity 99.8%; Pred. No. 6.7e-238; Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Qy 99 CAGGGGGAGCGGCAACGAGGAGCACTTCTGGAGACCACAACGACTCCTCTGGAA 158	Qy 159 GACGCTTGGGAGCAAGAGGTGCAAGTGCTGCCCCCTGCTTCCCTGCTGCAGGGGAG 218	Oy 219 CGGCAAGACAACGIGGGCGCTIGGGGAACTACGAIGACAGCGCCTICAIGGAICCCAG 278	OY 279 GTACCACGTCCATGGAGAACATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGGTAAAGT 338	Qy 339 CCCCAGAAAGGATCTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA 398	OY 399 AAAGAGGACTGCTCTACATCTGGCCATTGGGGAATTCAGAAGTAGTAAAACTCGT 458	Qy 459 GCTGGACAGATGTCAACTTAATGTCCTTGACAAAAAAGAGACAGCTCTGACAAA 518 Db 1131 GCTGGACAGACGATGTCAACTTAATGTCCTTGACAAAAAAAA	Qy 519 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC 578

CTGGATAGATATGGAAGAACTGCTTCATACTTGC 818 GTGCGTTAATGTTGCTGGAACATGGCACTGATCC 1250 ACCACTCTACACTATGCTGTACAATGAAGATAA 638 1, GAGAGTATGCTGTTTCTAGTCATCATCATG 933 Gaps ONS AND METHODS FOR THE AND DIAGNOSIS OF BREAST CANCER ; 819.8; DB 3; Length 1851; No. 2.5e-234; smatches 2; Indels 1; ole MS-DOS He #1.0, Version #1.30 32 210121 (419C3 oup Suite 6300 /991,789A 10: 291: Ą

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Query Match
Best Local Similarity 99.6%;
Matches 832; Conservative
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; ORGANISM: Homo sapien
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RESULT 10
US-09-439-313-366/c
; Sequence 366, Application US/09439313
; Patent No. 6229505
; GENERAL INFORMATION:
; APPLICANT: W. Jianghun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Read, Steven G.
; APPLICANT: Read, Steven G.
; APPLICANT: Fanger, Michael
; APPLICANT: Fanger, Michael
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John

1022 7; 158 218 903 338 843 398 783 458 638 698 758 423 818 363 878 303 963 518 663 578 603 543 483 723 1081 CAGGGGGACCGCCAAGAGCAACGTGGGCACTTCTGGAGACCACAAACGACTCCTCTGTGAA GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC 602 AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA 422 CAAGAAAAAGGGAATTTAAATGGGCTGGATAAGATATGGAAGAACTGCTCTCATACTTGC GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGAGCTGCCTGGTGGGGTAAAGT GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGACAAA AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAAAGCATGG ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAAACAAGCATGG 482 CCTCACACCCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAAGTGCTCTCATACTTGC TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAAACTCGT CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGGAG GGCCGTACAATGCCCAGGAAGATGATGTGCGTTAATGTTGCTGGAACATGGCCACTGATCC Gaps TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933 248 TTCTCAAGATCTGGAAAAGACGGCCAGAGGTATGCTTTTCTAGTCATCATG 1, Length 1851; APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT PEPLICATION WUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: SELEEQ for Windows Version 3.0
LENGTH: 1851 Indels DB 4; 7 Score 819.8; DB 4; Pred. No. 2.5e-234; 0; Mismatches 2; 542 669 759 819 879 a ò 셤 ò g ઠે g à

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TYPE: nucleic acid
STRANDEDNESS: single
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US-09-062-451-292
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US-09-062-451-292/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGAG
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               Sequence 291, Application US/09062451
| Patent No. 6344550
| Fatent No. 6344560
| GENERAL INFORMATION:
| APPLICANT: Frudakis, Tony N. APPLICANT: Smith, John M. APPLICANT: Read, Steven G. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES:
| NUMBER OF SEQUENCES: ADDRESS: ADDRESS: ADDRESSE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1851;
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                                                                                                                                                                                                                                                                            COUNTY: USA
COUNTY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN RCHEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FTLING DATE: 04-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.9%; Score 819.8; DB 4; Best Local Similarity 99.6%; Pred. No. 2.5e-234; Matches 832; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.419C2
TELEPCOMMUNICATION INFORMATION:
TELEPAK: (206) 682-6930
TELEFAK: (206) 682-6931
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TENGTH: 1851 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
US-09-062-451-291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC 878
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                                                                                                                                                                                                                                                                                                                                                                                            579 AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCATACTTGC
                                                                           519 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC
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Sequence 29.3 Application US/09062451

Sequence 29.3 Application US/09062451

Settent No. 634450

GENERAL INFORMATION:

APPLICANT: Frudamith, John M.

APPLICANT: Reed, Steven G.

TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297

CORRESPONDENCE ADDRESS:

ADDRESSES: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
COUNTRY: USA

COUNTRY: USA

ZIP: 98104-709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 04-APPL 1997

CHASSIFGATION COMPATION:

APPLICATION NUMBER: USO 962,451

FILING DATE: 04-APPL 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
RELECOMMUNICATION INFORMATION:
TELEFONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
```

1022 218 818 878 AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT 458 638 698 758 363 963 278 903 338 843 398 783 578 603 543 483 423 GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAATGTTGATGTATCT GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGCACACGATCC GGCCCTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA 362 IGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC GACGCTTGGGAGGAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGGAG GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCA-GGGAG CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC CAGGGGAACGCCAAACGTGGGCACTTCTGGAGACCACACACGACTCCTCTGTGAA CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG CAGGGGGGGCGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTGTGAA TICTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTCTAGTCATCATCATG 933 Gaps ij Length 1851; Score 819.8; DB 4; Length Pred. No. 2.5e-234; O; Mismatches 2; Indels Query Match
Best Local Similarity 99.6%;
Matches 832; Conservative 1081 1021 782 819 66 159 219 962 279 902 339 842 399 459 722 519 662 579 602 669 482 759 422 879 ď 8 6 8 6 ठ व ठ g 8 8 8 S 8 8 8 6 2 8 2 8 8 B 8 셤 8 8

TUL - 545-0/5T-8/0-0T-80

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Mon May

RESULT 13
US-09-352-616A-366/C

US-09-352-616A-366/C

SQUENCE 366, Application US/09352616A

PATENT NOT SQUENCE 366, Application US/09352616A

GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Vu, Jianghohun.
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham Jennifer Lynn
APPL

1022 158 963 903 843 783 458 723 578 638 543 698 483 758 423 818 363 878 663 603 962 CGGCAAGGAACGTGGTCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG CAAGAAAAAGGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAATGTTGATGTATC CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC AAATATTCCAGATGAGTATGGAAATAÇCACTCTACACTATGCTGTCTACAATGAAGATAA CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC Gaps 248 .; H Query Match 87.9%; Score 819.8; DB 4; Length 1851; Best Local Similarity 99.6%; Pred. No. 2.5e-234; Matches 832; Conservative 0; Mismatches 2; Indels 1; THEIR TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR 'PILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT PILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 366
LENGTH: 1851 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-352-616A-366 819 1081 219 902 842 399 782 459 662 579 602 542 669 722 639 482 759 422 362 879 99 279 339 519 g 요 장 g ઠ 셤 ઠે g ò 셤 셤 g ò a ઠે 셤 දි දි ò g ठ 8 8 ö 8 ઠે

482 422 362 879 669 759 819 g g ð 셤 ઠે 셤 ò 셤 8 상 음 $\dot{\delta}$ ઠે ઠે g ò 1022 158 218 843 398 963 278 458 783 723 722 GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAAGAGGACAGCTCTGACAAA 663 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC 578 603 AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA 638 543 159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCTGCTTCCCCTGCTGCAGGGGAG CAGGGGAGCGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCGCTTCATGGATCCCAG 902 GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT 339 CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACGGATGTGAACAAGAGGGACAAGCA AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAAAACTCGT GCCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC 399 AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT Gapa Ξ, Length 1851; S FOR THE OF BREAST CANCER Indels Query Match 87.9%; Score 819.8; DB 4; Best Local Similarity 99.6%; Pred. No. 2.5e-234; Matches 832; Conservative 0; Mismatches 2; RESULT 14
US-09-289-198-291/C
Sequence 291, Application US/09289198
Fatent No. 6586570
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF B FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
CURRENT FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-04-09
EARLIER FILING DATE: 1997-04-09
EARLIER FILING DATE: 1997-04-09
EARLIER FILING DATE: 1997-04-09
EARLIER FILING DATE: 1996-08-09
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FeatSEQ for Windows Version 3.0
LENGTH: 1851
TYPE: NNA TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-291 219 ტ ტ 1081 279 842 782 459 662 579 d 상 음 당 g ò g ò g ò ò a ò 임 ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT 338
                                                                                                                                           818
                                                                                                                                                                                    363
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                483
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                                                                                  CAAGAAAAAGGGAATTTAAATGGGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC
                                                                                                                                                                                                                                                       TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-289-198-292/c

j Sequence 292, Application US/09289198

patent No. 6586570

GENERAL INFORMATION:

j APPLICANT: Fridakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Mith, John M.

APPLICANT: Mith, John M.

APPLICANT: Mith, John M.

APPLICANT: Mith, John M.

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST

CURRENT FILING DATE: 1190-04-09

CURRENT FILING DATE: 1999-04-09

EARLIER FILING DATE: 1999-04-17

EARLIER FILING DATE: 1999-12-11

EARLIER FILING DATE: 1997-04-09

EARLIER FILING DATE: 1997-04-09

EARLIER FILING DATE: 1997-04-09

EARLIER FILING DATE: 1997-04-09

EARLIER FILING DATE: 1997-01-01

EARLIER FILING DATE: 1996-08-20

EARLIER FILING DATE: 1997-01-10

EARLIER FILING DATE: 1996-01-01

WUMBER OF SEQ ID NOS: 312

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH 1851

PURCH.
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87.9%; Score 819.8; DB 4;
Best Local Similarity 99.6%; Pred. No. 2 5e-234;
Matches 832; Conservative 0; Mismatches 2;
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Search completed: April 30, 2004, 13:09:24 Job time : 99 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Gapop 10.0, Gapext 1.0 Searched: 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: 6940544 Minimum DB seq length: 200000000 Post-processing; Minimum Match 1008 Listing first 45 summaries Database: GenEmbl:* 1 gb ba:* 2 gb lin:* 4 gb con:* 5 gb con:* 5 gb con:* 1 gb ba:* 1 gb ba:* 1 gb ba:* 2 gb lin:* 4 gb con:* 1 gb con:* 1 gb con:* 2 gb lin:* 1 gb con:* 2 gb lin:* 1 gb con:* 2 gb lin:* 4 gb con:* 5 gb con:* 5 gb con:* 6 gb con:* 1 gb con:* 1 gb con:* 2 gb con:* 3 gb con:* 3 gb con:* 4 gb con:* 5 gb con:* 6 gb co	37: em_htg_vrt:* 38: em_sy:* 39: em_trg_vhm:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•	Description	61059 Sequen	AR367286 Sequence	AR400322 Sequence	AR405589 Sequence	AX433323 Sequence AX141041 Sequence	AX200901 Sequence	AX267557 Sequence	AASIB977 Sequence AR261058 Sequence	AR278589 Sequence	AR367285 Sequence	AR4003ZI Sequence	AR433322 Sequence	AX141040 Sequence	AX200900 Sequence	AX282954 Sequence	AX316976 Sequence	AR148112 Sequence	Sequence	AR278471 Sequence	AR350934 Sequence	AR367167 Sequence	AR371063 Sequence	AR400203 Seguence AR405470 Seguence	AR433310 Sequence	AR433311 Sequence	AXIODOSO SEGUENCE AXIAOS76 Seguence	AX200736 Sequence	AX267392 Sequence	AXZ82952 Sequence	າເກ	Composi	Composit	BDZ4ZZ68 COMPOUNDS	Sequenc				linear PAT 29-JAN-2003	.0					engine mounted in vehicle
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AR278590 Sequence 531 from patent AR278590 AR278590.1 GI:29712836

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ISM Unknown.

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(E 1 (bases to 879)

NR Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Ralos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

E Compositions and methods for the therapy and diagnosis of prostate cancer

Concert US 6512094-A 531 28-JAN-2003;

RES

Location/Qualifiers

Source | corganism="unknown" |

Mol_type="genomic DNA" |
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                                                        AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT
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Retter,M.W. and Dillon,D.C.
Compositions and methods for the treatment and diagnosis cancer
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Pred. No. 7.4e-196;
0; Mismatches 2; Indels 0
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Location/Qualifiers
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Sequence 314 from patent US 6656480.
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/organism="unknown"
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1 (bases 1 to 879)

1 (bases 1 to 879)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.P., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                            CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCT
                       1 Similarity 99.8%; Score 831.8; DB 6; Similarity 99.8%; Pred. No. 7.4e-196; 33; Conservative 0; Mismatches 2;
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAAGT
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CORIXA CORPORATION (US)
Location/Qualifiers
1. .879
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 531 from Patent WO0134802.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meadper, M.J. Stolk, J.A., Skeiky, Y.A., Wang, A. and Meadper, M.J. Compositions and methods for the therapy and diagnosis of prostate cancer. CORIXA CORPORATION (US) 1. 879 / Organism="Homo sapiens" // Organism="Homo sapiens" // Ab_xref="taxon:9606"	9.2%; Score 831.8; DB 6; Length 879; 9.8%; Pred. No. 7.4e-196; ve 0; Mismatches 2; Indels 0; Gaps 0;	CAGGGGGAGCGGCAAACGTGGGCACTTCTGGAGACCACAAGGACTCCTGTGTAA 158	GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCTGCTGCTGCTGCTGCGGGGGAG 218	CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG 278	GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCTGGTGGGGGTAAAGT 338	CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA 398	AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT 458	CTGGACAGACGATGTCCAACTTAATGTCCTTGACAACAAAAGAGGACAGCTCTGACAAA 518 	GGCCGTACAATGCCAGGAAGATGAGATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC 578	AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA 638 	ATTRATGGCCAARGCACTGCTCTTATACGGTGCTGATATGAATCAAAAAAAAA	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT 758	CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818 	IGTATGTIGTGGATCAGCAAGTATAGTCAGCCCTCTACTIGAGCAAAATGTIGATGTATC 878 	
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0173032-A 531 04-OCT-2001;
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Location/Qualifiers ö 26-OCT-2001 161 338 341 218 398 278 221 281 458 401 518 461 578 521 638 581 698 Homo sapiens Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 399 AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT
342 AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT 876 0; Gaps linear PAT Length 879; 2; Indels Query Match 89.2%; Score 831.8; D3 6; Best Local Similarity 99.8%; Pred. No. 7.4e-196; Matches 833; Conservative 0; Mismatches 2; AX267557 879 bp DNA Sequence 531 from Patent WO0173032. AX267557 AX267557.1 GI:16516281 1. .879 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 322 579 522 639 RESULT 9
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Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps ORIGIN

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JOURNAL Patent: US 6329505-A 530 11-DEC-2
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TITLE Compositions and methods for therapy and diagnosis of pros cancer JOURNAL Patent: US 6329505-A 530 11-DEC-2001;
Day, C.H. TITLE Compositions and methods for therapy and diagnosis of prostat cancer cancer Patent: US 6329505-A 530 11-DEC-2001;
Red, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. Day, C.H. TITLE Compositions and methods for therapy and diagnosis of prosta cancer JOURNAL Patent: US 6329505-A 530 11-DEC-2001;
1 (bases 1 to 1852) Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. a Day,C.H. Compositions and methods for therapy and diagnosis of prostat cancer. US 6329505-A 530 11-DEC-2001;
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	REFERENCE AUTHORS	- KKY	1 (bases 1 to 1852) Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
	TITLE	P O	pier, w.r. and methods for the therapy and diagnosis of prostate prostate
	JOURNAL FEATURES SOUIC		Lent: US 6620922-A 530 16-SEP-2003; Location/Qualifiers 11852
	ORIGIN		/organism="unknown" /mol_type="genomic DNA"
	Query Match Best Local Sim Matches 833;	atch sal S 833	89.2%; Score 831.8; DB 6; Length 1852; imilarity 99.8%; Pred. No. 7.4e-196; ; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	δλ	9	CAGGGGGAGGGGCAAGGTGGGGCACTTCTGGAGACCACACGACTCCTGTGAA 158
	qa	171	CTGGAGACCACAAGGACTCCTCTGTG
	8	159	GACGCTTGGGAGCAAGAGAGATGCAAGATGCCACTGCTTCCCCTGCTGCAGGGGGAG 218
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	od da	1431	CAAGAAAAAGGGAATTTAAATGGGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 1490
	ŏ	819	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC 878
	eg G	1491	TGTATGTTGTGGATCAGCAAGTATGAGCCCTCTACTTGAGCAAATGTTGATGTATC 1550
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89.2%; Score 831.8; DB 6;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2;
                                                AR405588 1852 bp DNA
Sequence 530 from patent US 6630305.
AR405588 GI:40154425
                                                                                                                                                                                                                                                                                                                                                                                 cancer
Patent: US 6630305-A 530 07-OCT-2003;
Location/Qualifiers
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/organism="unknown"
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KEYWORDS
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QY 819 TGTAATGTTGGAATCAGCAAGAATATGATCAGCCTCTACTTGAGCAAAATGTTGATGTTATC 878

Db 1491 TGTATGTTGGAATCAGCAAGTATAGTCAGCCTCTACTTGAGCAAATGTTGATGTTATC 1550

QY 879 TTCTCAAGATCTGGAAAGACGCCAGAAGATATCTTCTAGTCATCATCATG 933

Db 1551 TTCTCAAGATCTGGAAAGACGCCAGAAGATATCTTCTAGTCATCATCATG 933

Db 1551 TTCTCAAGATCTGGAAAGACGCCAGAAGATATCTTCTAGTCATCATCATG 1605
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Search completed: April 30, 2004, 12:25:17 Job time : 3751 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- nucleic search, using sw model OM nucleic April 30, 2004, 10:10:26; Search time 426 Seconds (without alignments) 9304.152 Million cell updates/sec

Run on:

US-10-079-137B-343 933 1 atggtggttgaggttgattc......tgtttctagtcatcatcatg 933

Title: Perfect score:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

3373863 seqs, 2124099041 residues Searched:

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Database :

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1. geneseqn1990s:*

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	Description		Adc15395 Human bre	Adc15396 Human bre	Abt43733 Molecule	Adc15394 Human bre	Adc15393 Human bre	Aac81016 Human bre	Aah93826 Human pro	9 Human	Aah85140 Human pro	Aca59727 Prostate	Ab195290 Human B30	Aas99862 Breast tu	Acc95454 Prostate	Ada11393 Human bre	Adc15366 Human bre	Adb13981 Human pro	5 Human	Aah93825 Human pro	Aai67210 B305D iso	Aas63918 Human pro	Aah85139 Human pro	3726 Prosta	Ab195289 Human B30
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ALIGNMENTS

RESULT 1

Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; Human breast tumour protein DNA, SEQ ID 343. BP. 05-AUG-2002; 2002WO-US024917. ADC15395 standard; DNA; 933 (first entry) WO2003013431-A2 sapiens. 18-DEC-2003 20-FEB-2003 ADC15395; Ношо ADC15395

07-AUG-2001; 2001US-00924400. 20-FEB-2002; 2002US-00079137. 02-AUG-2002; 2002US-00212679.

Foy TM, Houghton RL, Dillon DC, Fanger GR, Hirst SK, Kalos MD;

(CORI-) CORIXA CORP

Persing DH;

New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer. WPI; 2003-342398/32.

Claim 1; SEQ ID NO 343; 308pp; English.

The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells

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                                                                              Sequence 933 BP; 272 A; 201 C; 248 G; 212 T; 0 U; 0 Other;
        present sequence was
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                                                                                                                              Query Match
100.0%; Score 933; DB 9; L. Best Local Similarity 100.0%; Pred. No. 6.3e-269; Matches 933; Conservative 0; Mismatches 0;
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The present invention relates to compositions and methods for the therapy detecting the presence of a cancer in a patient concer. The method for biological sample from the patient, contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent, and comparing the amount of the polypeptide to a predetermined cut-off comparing breast cancer comprises administering a composition comprising breast specific for the tumour proteins and nucleic acids, which simulates and/or expands T cells specific for the tumour protein. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
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                                                                                                                                                                                                                                                                                              Cytostatic, Gene therapy; breast cancer; breast tumour protein; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGGAGCAAGATGGCGAGTGGTGCTGCCACTGCTTCCCTGCTGCAGGGGGGAGCGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for preparing a composition for diagnosing,
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                                                                                                                                                                                                                                        SEQ ID 344
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20-FEB-2002; 2002US-00079137.
02-AUG-2002; 2002US-00212679.
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13-JUL-2001, 2001US-0305324P. 19-JUL-2001, 2001US-0307003P. 27-JUL-2001, 2001US-0308185P. 03-AUG-2001, 2001US-0310096P. 10-AUG-2001, 2001US-031551P. 08-MAR-2002; 2002US-0363649P.

(INCY-) INCYTE GENOMICS INC

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New Molecules for Disease Detection and Treatment polypeptides, useful for preparing a composition for diagnosing or treating e.g. cardiovascular or neurological disorders.

WPI; 2003-533003/50, P-PSDB; ABJ39131.

Claim 5; Page 276; 289pp; English.

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Thornton M, Au-Young JK, Azimzai Y, Bandman O, Barroso I; Budgm MR, Becha SD, Borowsky ML, Ding L, Duggan BM, Elliott W. Emerling BM, Forsythe IJ, Gandhi AR, Gietzen KJ, Gorvad AE; Griffin JA, Gururajan R, Hafalia AJA, Ring HZ, Ison CH, Jones Lial PG, Lee EA, Lee S, Li JX, Lu DAM, Marquis JP, Lehr-Mason Clal PG, Lee EA, Ley Janwala B, Sornasse I, Swarnakar A; Tang YT, Thangavelu K, Tran B, Tran UK, Warren BA, Xu Y, Yao Yue H, Yue H, Zebarjadian Y, Chang H;

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ABT43733 standard; cDNA; 1689
         (first entry)
ABT43733
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Human; Molecules for Disease Detection and Treatment; MDDT; MDDT-antagonist; MDDT-agonist; Gene therapy; cardiant; cytostatic; neuroprotective; cardiavosacular disorder; neurological disorder; cell proliferative disorder; autoimmune disorder; inflammatory disorder; developmental disorder; cancer; steroid metabolic response; gene; ss. Molecule for disease detection and treatment (MDDT)-41 cDNA sequence

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09-JUL-2001; 2001US-0304298P.
                              WO2003052049-A2
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This invention relates to novel polypeptides associated with Molecules for Disease Detection and Treatment (MDDT) and the cDNA sequences which encode them. MDDT-antagonists, MDDT-agonists or gene therapy may produce cardiant, cytostatic and neuropyrotective activities. The polypeptides and composition for the diagnosis or treatment of a disease which is associated with decreased expression or over-expression of functional MDDT proteins, for example cardiovascular, neurological, cell proliferative, autoimmune/inflammatory or developmental disorders. They may also be useful in the treatment and diagnosis of cancer, diseases treated with steroids and disorders caused by the metabolic response to treatment with steroids. The present sequence is the cDNA sequence encoding a human Molecule for Disease Detection and Treatment (MDDT) of
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New polynucleotide, useful for preparing a composition for diagnosing

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The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for beteeting the presence of a cancer in a patient comprises the partial of a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample and amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast undour proteins and nucleic acids, which simulates and/or expands I cells specific for the tumour protein. The present sequence was used to
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89.5%; Score 835; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-239;
Matches 835; Conservative 0; Mismatches 0;
                           Claim 1; SEQ ID NO 342; 308pp; English.
 treating or preventing cancer
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                    GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT
                                                             CCCCAGAAAGGATCTCATGGTCATGCTCAGGGACACTGATGTGAACAAGAGGACAAGCA
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breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
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28-OCT-1999; 99US-00429755.
23-MAR-2000; 2000US-00534825.
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23-MAR-2000;
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                                                                                                                                                                                                                                                            Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynuclectide, useful for preparing a composition for diagnosing, treating or preventing cancer.
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                      TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG
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Pred. No. 1.4e-238;
0; Mismatches 2;
                                                                                                                                                                                                                              Human breast tumour protein DNA, SEQ ID 341.
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20-FEB-2002; 2002US-00079137.
02-AUG-2002; 2002US-00212679.
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99.8%;
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Best Local Similarity 99.8
Matches 833; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-342398/32
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                                                                                                                                  ADC15393 standard;
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CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC

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WPI; 2000-628403/60.
P-PSDB; AAB28636.
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An isolated polypeptide comprising an immunogenic portion of a breast tumor protein used for inhibiting the development of cancer, especially breast cancer, and monitoring cancer progression in a patient. Claim 4; Page 185-186; 187pp; English.

The present sequence is given in a specification relating to compositions and methods for the treatment and diagnosis of breast cancer. Nucleotide sequences that are preferentially expressed in breast tumour tissue, and compositions and vaccines to inhibit the development of cancer, especially breast cancer. The progression of a cancer may be monitored by carrying out detection of tumour-specific antiqens at subsequent time points and comparing the results from the different time points. CD4+tumour-specific antiqens at subsequent time tumour-specific polypeptides, polynucleotides encoding the polypeptides or antigen presenting cells expressing the polypeptides or antigen presenting cells expressing the polypeptides are then administered to the patient to inhibit development of cancer

Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

g ò g

ö 458 518 578 638 581 698 758 701 158 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGAG 218 278 221 338 281 398 341 401 461 521 CAGGGGGACCACAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCTCTGTGAA 101 161 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC cercacaccacracractracaracaraaccaaaaacaccaagracacaaarrrraar CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA GACGCTTGGGAGGAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGAAG COCCAAGAGGAACGTGGGGGGGGGAGACTACGATGACAGGGGCCTTCATGGATCCCAG CGGCAAGAGCAACGTGGTTGGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGGTAAAGT CCCCAGAAAGGATCTCATGGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACGGATGTGAAGAACAAGGA AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT gcrogacagacagargrcaacrraargrccrrgacaacaaaaaagaggacagcrcrgacaaa AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGGTAAAGT GGCCGTACAATGCCAGGAAGATGAGAGTTAATGTTGCTGGAACATGGCACTGATCC Gaps ö Length 879; Indels 89.2%; Score 811.8; DB 3; llarity 99.8%; Pred. No. 1.4e-238; Conservative 0; Mismatches 2; Local Similarity ses 833; Conserv 399 402 462 639 342 459 519 579 522 582 669 219 222 282 642 66 42 159 102 162 279 339 Query Match Best Loca Matches

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The present invention describes polymucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (I), (II) tusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The ankibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapautic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
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                                                                                                                                                                                                                                                                                                       Human prostate-specific cDNA sequence splice variant open reading frame.
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CAAGAAAAAAGGGAATTTAAATGCGCTGGATAGATATGGAAGAAGAACGCTCTCATACTTGC
                                         TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
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                                                                                                                                                                                                                                                                                                                                        Human, prostate cancer, prostate-specific, diagnosis, vaccine; cytostatic, gene therapy, metastasis, ss.
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Retter MW, Stolk JA, Skeiky
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99.8%; Pred. No. 1.4e-238;
ative 0; Mismatches 2;
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3R, Day CH,
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                                                                                                                                                                                                                AAH93826 standard; cDNA; 879
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Wang A, Meagher MJ;
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ğö Kalos M Carter

27-MAR-2000; 2000US-00536857.
09-MAY-2000; 2000US-00568100.
12-MAY-2000; 2000US-00550137.
13-UJN-2000; 2000US-0055793.
27-UJN-2000; 2000US-0065783.
09-MUG-2000; 2000US-0063783.
06-SEP-2000; 2000US-00657236.
02-OCT-2000; 2000US-00679426.
10-OCT-2000; 2000US-00679426.

(CORI-) CORIXA CORP.

Χu J,

2001WO-US009919

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멾 AAS63919 standard; cDNA; 879 AAS63919;

29-JAN-2002

Human prostate cDNA clone B305D splice variant #11 open reading Human; prostate cancer; 88; cytostatic; immunostimulant; tumour (first entry) Homo sapiens

WO200173032-A2 04-OCT-2001

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GCTGGACGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGACAAA

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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention 158 218 398 282 CCCCAGAAAGGAICTCAICGICAIGGICAGGGACACGGAIGIGAAGAACAAGAGGACAAGGA 341 458 101 102 ekceciriesekacekadadarecakerederecekerecekeriederederedagaseka 161 221 281 401 for CGGCAAGAAGGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG 162 CGGCAAGAGCAACGTGGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT 339 CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA 399 AAAQAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT 99 CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA 42 caggoggagcogcaagagcaacgrooggaacrrcrosagaaccacaacgacrccrcrororaa 342 AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT Gaps New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer. ; 0 89.2%; Score 831.8; DB 4; Length 879; 99.8%; Pred. No.1.4e-238; ive 0; Mismatches 2; Indels 0; Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other; Harlocker SL, Jiang Y, A, Day CH, Vedvick TS, spler WT, Henderson RA; Dillon DC, Mitcham JL, Harlocker GR, Retter MW, Stolk JA, Day CF Wang A, Skeiky YAW, Hepler WT, Claim 1; Page 408; 579pp; English. Query Match
Best Local Similarity 99.8
Matches 833; Conservative WPI; 2001-639232/73. P-PSDB; AAU69821. Fanger GR, Rette Li SX, Wang A, 279 (219 g ď ð 요 8 g 쉱 à g δ ઠે

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521 638 581 698 641 758 701

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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymuclectides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The
GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGAGACAGCTCTGACAAA
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                                                                                                                GCCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC
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Day CH, Skeiky YAW,
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Kalos MD, Retter MW, Stolk JA,
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polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes PrO4P, PT2P, PT4P, pT75P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. ARM84671 to AAM85143 and AAG99000 to AAG99077 represent polymucleotide and polypeptide sequences used in the exemplification of the present invention
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89.2%; Score.831.8; DB 4;

Best Local Similarity 99.8%; Pred. No. 1.4e-238;

Matches 833; Conservative 0; Mismatches 2;
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Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

segdata.uspto.gov/seguence.html?DocID=US20020192763

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The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from the US patent office at Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer. Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA; gene; ss. Kalos MD; Carter D; Hural J; Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retteer MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skelky YaW, Hepler WT, Henderson RA, Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM, Prostate cancer therapy associated cDNA #464 Example 11; SEQ ID NO 531; 85pp; English. ВР ACA59727 standard; cDNA; 879 04-OCT-1999; 99US-0157455P. 04-OCT-2000; 2000US-00679272. 28-MAR-2001; 2001US-00822827. 29-JUN-2001; 2001US-00895793 MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M. (first entry) XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L. LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T. JIANG Y.
KALOS M D.
FANGER G R.
STOLK J A.
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CENTER D. WPI; 2001-245062/25 HURAL J. US2002192763-A1. Homo sapiens. 10-JUN-2003 19-DEC-2002 ACA59727 (DILL/)
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Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy; gene; ss.
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10-FEB-1997; 97US-00904804.
10-FEB-1998; 98US-00030567.
25-FEB-1998; 98US-00015556.
23-SEP-1998; 99US-001155812.
15-JAN-1999; 99US-00132149.
15-JAN-1999; 99US-00232149.
12-NOV-1999; 99US-00352616.
12-NOV-1999; 99US-00352616.
13-JUL-1999; 99US-00352616.
14-JAN-2000; 2000US-00439313.
17-MAR-2000; 2000US-0043686.
13-JUN-2000; 2000US-00536857.
27-JUN-2000; 2000US-0053687.
13-JUN-2000; 2000US-0053193.
13-JUN-2000; 2000US-0053193.
10-AUG-2000; 2000US-0053193.
10-AUG-2000; 2000US-00551216.
29-AUG-2000; 2000US-00551216.
10-OCT-2000; 2000US-00651216.
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DILLON D C.
MITCHAM J L.
HARLOCKER S L.
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Kalos MD; Carter D; Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.

Claim 1; SEQ ID NO 531; 87pp; English.

The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention

Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

ö 458 101 159 GACGCTTGGGAAGCAAGAGGTGCAAGTGCTGCCACTGCTTCCCCTGCTGCTGCAGGGGAG 218 278 398 518 578 638 878 221 281 401 461 521 698 758 761 821 581 641 701 CGGCAAGAGCAACGTGGTCGCTTGGGGAACTACGATGACAGCGCCTTCATGGATCCCAG TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC CAGGGGAAGGGAAGAGCAACGTGGGCACTTCTGGAGACCAACGACTCCTCTGTGAA GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT GTACCACGCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGGTAAAGT GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAAGAGGACAGCTCTGACAAA 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAACAAGCATGG CAAGAAAAAGCGAATITAAATGCGCTGGATAAGATATGGAAGAACTGCTCTCATACTTGC 99 CAGGGGAGCGCCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAACAAGCATGG CCTCACACCACTGCTACTTGCTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATC 933 Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant; tumour; vaccine; immunogenic. ; 0 Length Indels Score 831.8; DB 6; Pred. No. 1.4e-238; 0; Mismatches 2; Breast tumour-specific ORF B305D isoform A. B Query Match
Best Local Similarity 99.8%;
Matches 833; Conservative AAS99862 standard; DNA; 879 219 162 279 339 519 282 459 402 462 759 762 879 AAS99862; 셤 ò g ò g ò 임 à 셤 ò 유 ò 셤 ò g à g g ઠે g ò ઠે 요 g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to novel prostate-specific proteins (PSP)
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                                462 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC
                                                                                                                                               ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAAACAAGCATGG
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GGCCGTACAATGCCAGGAAGATGAATGTGCGGTTAATGTTGCTGGAACATGGCACTGAATCC
                                                                                                           AAATATICCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic, gene therapy, prostate-specific protein, PSP; human, immune response; prostate cancer; ss.
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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Mcneill PD,
Deng T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel breast tumour polynucleotides and polypeptides. The polypeptides and polynucleotides are useful in pharmaceutical compositions for treating and/or preventing cancer, particularly breast cancer, and for eliciting an immune response, particularly humoral and/or cellular immune response. The polynucleotides may be used as probes or primers for nucleic acid hybridisation, in the design and preparation of riboxyme molecules for inhibiting expression of tumour polypeptides and proteins, and in recombinant DNA molecules to direct expression of a polypeptide in host cells. AAS99570-AAS99888 represent novel human breast cancer protein coding sequences and PCR primers of the invention
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                                                                                                                                                                                                                                                                                     Dillon DC,
                                                                                                                                                                                                                                                                                     Harlocker SL, Day CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 231-232; 245pp; English
                                                                                                                                               24-WAY-2000; 2000US-00577505.
08-JUN-2000; 2000US-00590583.
26-OCT-2000; 2000US-00699295.
16-WAR-2001; 2001US-00810936.
                                                                                                               22-MAY-2001; 2001WO-US016776
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Skeiky YAW,
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P-PSDB; AAU74385.
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  Homo sapiens
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and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to illustrate the invention
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                                                                                             Score 831.8; DB 7;
Pred. No. 1.4e-238;
0; Mismatches 2;
                                                                         G; 201
                                                                         C; 222
                                                                                              Match 89.2%;
Local Similarity 99.8%;
les 833; Conservative
                                                                         Sequence 879 BP; 263 A; 193
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RESULT 14
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The invention relates to a breast tumour polymucleotide selected from one of the 275 fully defined nucleotide sequences (a) given in the second that it is the complements, sequences consisting of at least 20 contiguous residues of a sequence in (a), sequences that hybridise to a sequence in (a) under moderately stringent conditions, sequences having at least 75% or 90% identity to a sequence in (a), or sequences having at least 75% or 90% identity to a sequence and isolated polypeptide (II) (comprising an amino acid sequence selected from to a sequence encoded by (a), sequences of 30 fully defined amino acid sequences (c), and sequences having at least 70% or 90% identity to a sequence in (2), expression vectors comprising (a), a host cell cransformed or transfered with the expression vectors comprising (a), a host cell cransformed or transfered with the expression vector, an isolated antibody or its antigen-binding fragment that specifically binds to (II), a method for detecting the presence of a cancer in a patient, a fusion protein comprising at least one polypeptide (II) and oligomucleotide that hybridises to (a), under moderately stringent conditions, a method for stimulating and/or expanding T cells specific for a tumour protein (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New breast tumor proteins nucleic acids encoding such proteins, useful ir diagnosing, preventing and/or treating diseases such as cancer, particularly breast cancer, and as markers for detecting the presence of
                                                                                breast cancer; cytostatic; tumour; gene therapy
                                                 Human breast cancer specific full length cDNA B305D-A ORF
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10-JAN-1997; 97WG-US000485.
09-ARR-1997; 97US-00838762.
11-DBC-1999; 97US-00901789.
17-ARR-1999; 99US-00289198.
23-GCT-1999; 99US-00289198.
23-GCT-2099; 200UUS-0057655.
24-MAY-2000; 200UUS-0059083.
26-GCT-2000; 200UUS-00659295.
16-MAR-2001; 200UUS-0069395.
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contacting T cells with at least one component selected from (a), (II) and and antigen-presenting cells that express (II)), an isolated T cell population comprising T cells prepared from as detailed above, a method for stimulating an immune response or treating cancer in a patient by administering a composition comprising (a), (II), the vector, cells or the antibodies, and a method for inhibiting the development of a cancer in a patient. The polymorlectides may be used in the design and proparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells. The breast tumour proteins are useful as markers to indicate the presence or absence of a cancer, such as breast cancer, and in the detection of other cancers. Compositions preventing and/or treating diseases such as cancer. Darkers to indicate the presence or absence of a cancer, such as breast cancer. The present sequence is a breast cancer, particularly breast cancer. The present sequence is a breast cancer specific cDNA of the
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The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for betecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast themour proteins and nucleic acids, which simulates and/or expands I cells sillustrate the invention.
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Pred. No. 1.4e-238;
0; Mismatches 2;
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20-FEB-2002; 2002US-00079137.
02-AUG-2002; 2002US-00212679.
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99.8%;
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699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAGAGCAAGTGGTGAAATTTTTAAT 758
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                                                      CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGACAAGCA 398
                                                                            282 CCCCAGAAAAGGATCTCATCGTCATGCTCAGGGACACGCGATGTGAACAAGAGAGACAAGCA 341
                                                                                                               GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGACAAA 518
                                                                                                                                                                                                                                  GGCCGTACAATGCCAGGAAGATGAGTGCGTTAATGTTGCTGGAACATGGCACTGATCC 578
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Search completed: April 30, 2004, 11:22:37 Job time : 430 secs

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Manmalia; Butheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mukanyota; Metazoa; Chordata; Catarrhin; Hominidae; Homo.

1 (bases 1 to 61)

Kim,N.S.; Hahn,Y.; Oh,J.H.; Lee,J.Y.; Ahn,H.Y.; Chu,M.Y.; Kim,M.R.; Oh,K.J.; Cheong,J.B.; Sohn,H.Y.; Kim,J.M.; Park,H.S.; Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                    621, bp mRNA linear EST 04-MAR-2002
K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-A11 S',
mRNA sequence.
                                                                         BUSS 68215 AGENCOURT
BIR 71077 603394250
AKO84690 Mus muscu
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BK729652 RCG-EN027
BY717578 BY717578
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BC038951 Homo sapi
AA910780 O148b04.8
BC028407 Homo sapi
BM548157 AGENCOURT
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Korea Research Institute of Bioscience & Biotechnology
52 Beeun-dong Vuseong-gu, Daejeon 305-333, South Korea
TT-1: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621.
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                                                                   BMS48157
BUS68215
BI871077
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Homo sapiens
VERSION
KEYWORDS
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BM763453 K-EST0044
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                                                          April 30, 2004, 11:07:17 ; Search time 2524 Seconds (without alignments) 11038.595 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| organism="Immon sapiens"
| woll type="mRNA"
| woll xxef="taxon:9606"
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| clone="$\text{lone}$ | \text{saue}$ | \text{taxon:9610m} |
| clone | \text{lone}$ | \text{saue}$ | \text{taxon:9610m} |
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BM763453 633 bp mRNA linear EST 04-MAR-2002 K-EST0044791 S13KWS5 Homo Bapiens cDNA clone S13KWS5-16-All 5', RRNA sequence.
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Contact: Kim Wg.
Korea Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Bosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fax: +82-42-860-4409
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99.8%; Pred. No. 2,8e-125;
iive 0; Mismatchés 1;
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Plate: 16 row. A column: 11
High quality sequence stop: 633.
Location/Qualifiers
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Homo sapiens
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us-10-079-137b-343.rst

ORIGIN	Query Match 42.4%; Score 395.6; DB 13; Length 729; Best Local Similarity 90.5%; Pred. No. 8.9e-89; Matches 458; Conservative 0; Mismatches 14; Indels 34; Gaps 2;	Qy 462 GGACAGATGTCAACTTAATGTCCTTGACAACAAAAAGAGACAGCTCTGACAA 517 Db 3 GGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGACACTCTGATAAAGGT 62		QY 552 AATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATGAGAAATACCACTCT 611	Qy 612 ACACTATGCTGTCTACAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTATACGGTGC 671	Qy 672 TGATATCGAATCAAAAACAAGCATGGCCTCACACCACTGCTACTTGGTATACATGAGCA 731 Db 243 TGATATCGAATCAAAAAGCATGGCCTCACACCACTGTTACTTGGTGTACATGAGCA 302	Qy 732 AAAACAGCAAGTGGTGAAATTTTTAATCAAGAAAAAAGGGAATTTAAATGGCTGGATAG 791 Db 303 AAAACAGCAAGTGGTGAAATTTTTAATCAAGAAAAAGCGAATTTAAATGCACTGGATAG 362 Qy 792 ATATGGAAGAACTGCTCTCATACTTGCTGTAGTGTGGATCAGCAAGTATAGTGAGCCC 851 Db 363 ATATGGAAGACTGCTCTCATACTTGCTGTAGTTGTGGATCAGCAAGTATAGTCAGCCC 722	Oy 852 TCTACTTGAGCAAATGTTGATGTATCTTCTCAAGATCTGGAAAGACGGCCAGAGA 907	Qy 908 GTATGCTGTTTCTAGTCATCATCAGG 908 GTATGCTGTTTCTAGTCATCATCAGG 933 1	RESULT 4 BF676987 LOCUS BF676987 LOCUS DEFINITION 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5', MRNA sequence. ACCESSION BF676987 VERSYOND SF776987.1 G1:11950882	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: CLONETECH Laboratories, Inc.	cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Plate: LLCM1067 row: m column: 03 High quality sequence stop: 642. FEATURES Location/Qualifiers Source 1. 865 /organism="Homo sapiens"
Db 181 TGATCCAAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGA 240	Oy 633 AGATAAATTAATGGCCAAAGCACTGCTCTTATACGGTGGTGATATCGAATCAAAACAA 692	Oy 693 GCATGGCCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATT 752 Db 301 GCATGGCCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGATGAAATT 360	OY 753 TITAATCAAGAAAAAGCGAATITAAATGCGCTGGATAGATATGGAAGAACTGCTCCAT 812 Db 361 TITAATCAAGAAAAAAGCGAATITAAATGCGCTGGATAGATATGGAAGAACTGCTCCAT 420	Oy 813 ACTTGCTGTATCTTGTGGATCAGCAAGTATAGTCAGCCCCTCTACTTGAGCAAAATGTTGA 872	Oy 873 TGTATCTTCTCAAGAICTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCAT 932	Qy 933 G 933 Db 541 G 541	RESULT 3 BU930826 BU930826 T29 bp mRNA linear EST 18-OCT-2002 DEFINITION AGENCOURT 10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956 ACCESSION BU930826 ACCESSION HU930826	EST. Homo sapiens (human) Homo sapiens (homan) Thompselve (homan) Thompselve (homan)	Establication During Dutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 729) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)		http://image.llnl.gov Plate: LLCM2943 row: o column: 04 High quality sequence stop: 555. FEATURES Location/Qualifiers		/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site=1: Sfil (ggcgctcggct); Site=2: Sfil (ggccattatggct); 5, and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 6'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' 5'-ATTCTAGAGCCGAGGCGGCCGCCATTATGGC-4T(30)BN-3' (where B = A.	C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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/mol_type="mkNn"
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/dD_xref="texon:9606"
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/lab_host="labGE:4248746"
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/clone lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: postate; Vector: pDNR-LIB (Clontech);
/note="Organ: pDNR-LIB (Clon
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DKFZp781C0523_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DKFZp781C0523_5', mRNA sequence.
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EST (Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
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Matches 409; Conservative
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Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by GDE (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp781C0523) is available at the RZPD in Berlin.
This clone (DKFZp781C0523) is available at the RZPD in Berlin.
The clone (DKFZp781C0523) is available at the RZPD in Berlin.
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Homo sapiens cDNA clone CSOCAP006YL04
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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BX437445 Homo sapiens THYMUS HC
5-PRINE, mRNA sequence.
BX437445.
BX437445.1 GI:30771569
EST.
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AU120666
AU120666 HEMBB1 Homo sapiens cDNA clone HEMBB1001175 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AGAGCCGAGAGAGACATGAGGTCTCTGAAGCCCGGTCGCCTGGGCCATGAAGAAGATT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 GGGAGCAAGAGGTGCAGCTGCTGCCACTGCTTCCCCTGCTGCAGGGGGAGCGCCAAG 225
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 843)

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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1513-3 Yana, Kisarazu, Chiba 292-0812, Japan
1e1: 81-438-52-3975
Pax: 81-438-52-396
Email: genomics@hri.co.jp
HNI human cDNA project; 5.'- & 3.'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
       766 AAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGCTGTATGT
                                                                                                                    <u> AAAGCAAATGTAAATGCAGTGGATAAGTTGGAAAGCAGTCACCAACTAATTTCAGAATAT</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole embryo, mainly body"
dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pWE188FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/clone="HEMBB1001175"
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AU120666.1 GI:10935901
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Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
Homo sapiens
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCA-RO06FL04"
/tissue_type="THYMUS"
/clone="The mome sapiens THYMUS"
/note="Vector: pCNVSPORT 6, 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and SCORV sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequefospenoscope.ns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5500.r For
Invitrogen. This sequence belongs to sequence cluster 5500.r For
Intp://www.genoscope.cns.fr/
cgi.bln/cluster.cgi?seq=CSOCAPO06DF02QP1&cluster=5500.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPO06DF02QP1.
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Pred. No. 5.5e-77;
1; Mismatches 214; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.9%;
Matches 496; Conservative
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DKFZp686E1728_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686E1728_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Banis s.wiemann@dkfz- heidelberg.de,
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
ACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGTGCTGGAC 465
                      AGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGACAAAGGCCGTA 525
                                                                                                              470 AGAAAHGCCAGCICAATGTCTGTGACAACGAAAACAGGACAGCTCTGATGAAGGCTGTA 529
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                                                                                                                                                                                                                                  586 CCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAAATTAATG 645
                                                                                                                                                                                                                                                           590 GCGGATGTCCATGGCAACACACTGCTCTTCACTATGCTGTCTATAATGAGGACATATCAGTA 649
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                                                                                                                                                                                                                                                                                                                                                                                          CCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAATCAAAAA 765
                                                                                                                                                                                                                                                                                                                                                                                                                               710 ccacitriractificagiaagiegaaaaaaagcaccaaaregregradiririraataaagaaa 769
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 544)
Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="mRNA"
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/dev_stage="adult"
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/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZp686E1728) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                               GCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACA
                                                                                                                                                                                                                                                                                                                                          CAATGCCAGGAAGATGAGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST (Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      766 AAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    770 AAAGCAAATGTAAATGCCNTANATAAGTTGGAAAGCAGTCACCACTAATTT 820
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Unpublished (2001)
Contact: MIPS
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AUTHORS
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DB 9; Length 544;

35.5%; Score 331.2;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

El (Dases 1 to 1020)

NHH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Locality Sequence stop: 680.

High quality sequence stop: 680.
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone lib="DH10B (phage-resistant)"
/clone lib="NH MGC 92"
/note="Corgan: testis; Vector: pCMV-SPORT6; Site_l: NotI; Site_l: Sal1; Cloned unidix rectionally; oligo-dT primed.
Average insert size 2.5 %b. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGENCOURT 6444673 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585453
b/, mRNA sequence.
                                                                                                                                                                                                                                                                                                  GCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TIGCTIGGCGTGCATGAAAAAAAAAAGGGGAAATGAAAAATTTTTAATCAAGAAAAAAGCT 239
                                                                                                                                                                                          651
                                                                                                                                                                                                                                                                                                                                                       120 GCACTGCTCTTATATGGTGCTGATATTGAATCAAAAAAACAAGTGTGGCCTCACACCACTT 179
                                                                                                                                                                                                                                                                                                                                                                                                           771
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                                                                                                        1 CAGGAAGATGAATGTGTGTTAATGTTGCTGGAACATGGCGCCGATGGAAATATTCAAGAT
                                                                                                                                                                                                                          61 GAGTATGGAAATACCGCTCTACACTAT-CTATCTACAATGAAGATGAAATTAATGGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                           712 CTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAAATTTTTAATCAAGAAAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AATTTAAATGCACTTGATAGATATGGAAGAACAACTGCCCTCATACTTGCTGTATGTTGTGGA
                                                                              532 CAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGAT
                                                                                                                                                                                          592 GAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAAATTAATGGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      772 AATITAAAIGGGCIGGAIAGAIAIGGAAGAACIGCICICCAIACIIGCIGIAIGIIGIGGA
                               Gaps
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Pred. No. 1.4e-72;
0; Mismatches 28;
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BM469654.1 GI:18518696
Best Local Similarity 91.9%;
Matches 373; Conservative
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Homo sapiens
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AUTHORS
TITLE
JOURNAL
COMMENT
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cagaba-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgo@nbgri.nih.gov/
Contact: nisc.mgo@nbgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin.B.,
Blakeeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantipop,S., Thomman,J.W.,
TBURGEON,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be found
sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 GACTACGAIGACAGCGCCTICAIGGAICCCAGGIACCACGICCAIGGAGAAGAICTGGAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AAGCTCCACAGAGCTGCCTGGTGAGGTAAAGTCCCCAGAAAGGATCTCATCGTCATGCTC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adaricialidelerdecarcaaddecgacdecgegagarddagcacrocerdacdec 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAATGGGAATTCAGAAGTAGTAAAACTCGTGCTGGTGGACAGAGGTGTCAACTTAATGTC 486
                                                                                                                                                                                                                                                                                          Strausberg_R.
Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 82 Row: i Collum: il
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 GACTCCATGGACCAAGAGTACGCTGGTCGGGGTACCACATCCGGGACTGGGAACTGCGG
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Pred. No. 8.2e-58;
0; Mismatcheè 245; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
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Best Local Similarity 63.6%;
Matches 435; Conservative
                                                                                                                                                                                                                                                                      (bases 1 to 2285)
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 2285)

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Alschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S., Wang, J., Heieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Gascia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC038951 11-DEC-2003 HOMO Sapiens ankyrin repeat domain 19, mRNA (cDNA clone IMAGE:5733799), with apparent retained intron.
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                                                                                                                                                                                                                             CCACGTCCGAGACCGAGATCTCGGCAAGATCCACAAAGCTGCCAGCGGGGTAATGTGGC
                                                                                                                                                                                                                                                                                                342 CAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGCACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GGACAGAAATGCCAGCTCAATGTCTGTGACAAGGAAACAGGACAGCTCTGATGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTACAATGCCAGGAAGATGAGATGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAA
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                                                                                                                                                                                        282 CCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGTCCC
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                                                                                DB 12; Length 1020;
                                                                          Score 315.2; DB 12; Length
Pred. No. 2.1e-68;
0; Mismatches 143; Indels
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                                                                          33.8%;
al Similarity 73.7%;
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NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infe@image.llnl.gov) for further information. Insert Length: 1548 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 235.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mmRNA"
|db_xref="taxon:9606"
|clone="INAGE:152661"
|clone lib="Soares NFL T GBC S1"
|clone lib="Soares NFT"
|clone lib="Soares 
                                                                                                                                                                                                                                403 GCCATTATTCTCCTGGAACATGGCGCCAATCCAAACATTAAGGATATCTACAGCAACACT
                                                                                                                                                                                                                                                                                                                 607 ACTCIACACTATGCTGTACAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAATTICAGAAGAACAGCCCTCATGCTTGCAGTACAGCATAACTCATCAAGTATCGTC
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GCCCATGGCCGTGTGGAAGTGGTCACCCTCTTGCTGAGCAGAAGATGCCAGATCAACATA
                                                                                                                                                                                          547 GCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATGAGTATGGAAATACC
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                                                           487 CTTGACAACAAAAAGAGGACAGCTCTGACAAAGGCCGTACAATGCCAGGAAGATGT
                                                                                                                          343 TATGATAGACTAAACAGGACACCTTTAATGAAGGCTGTACACTGCCAGGAAGAGGCTTGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Is (bases 1 to 3443)

Strausberg, R.L., Feingold, E.A., Grouse, L.H.; Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Zordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellaho, N.A., Peters, G.J., Abramson, R.J., Mallek, J.A., Gunaratne, P.H., Richards, S.,
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vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 11.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Patima Bonaldo.
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                                                                                                                                                                                                                                                                                                 Length 539,
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Best Local Similarity 72.4%; Pred. No. 1.3e-55;
Matches 356; Conservative 0; Mismatches 135;
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Homo sapiens
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/tissue_type="httppocampus"
/tab_note="DHIDB"
/lab_hote="DHIDB"
/lone lib="NHIDB"
/lone lib="HIP Sale | Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: NOTI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (Ecory site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 bp mRNA linear EST 20-FBB-2002
AGENCOURT 6571417 NIH_MGC_124 Home sapiens CDNA clone IMAGE:5733799
EM548157
                                                                                                                                                                                                                                                                                                                                                                    607 CACACCCTTTTACTGGCCATACGGAAAGGAAGCAAGCAAACTGTGGAATTTTTACTAAC 666
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   582 TATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAAATT 641
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I (bases 1 to 1079)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Invitrogen

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LIML)

DNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

http://image.llm.gov

Plate: LiLAMI2738 row: b column: 08

High quality sequence stop: 632.
                                                                                                                                             487 trateraganeretateceaacaceeretecarraneceirrangeneaentreir
                                                                                                                                                                                                          822 ATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATCTTC

    1079
    /organism="Homo sapiens"
/mol_type="mRNA"
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Homo sapiens
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SOURCE
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help deek
Email: cgapbs.remail.nih.gov
Email: cgapbs.remail.nih.gov
Email: cgapbs.remail.nih.gov
Email: cgapbs.remail.nih.gov
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The First of Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sadergy, Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jonee, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length Human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23.APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 CATCTACTTCGGGGATCTAGGGAAGATCCATACAGCTGCCTCCCGGGGCCCAAGTCCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 GGACAGACGATGTCAACTTAATGTCCTTGACAAAAAAAAGGACAGCTCTGACAAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            finalysis
This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch
28.0%; Score 260.8; DB 11; Length
al Similarity 65.1%; Pred. No. 2.2e-54;
401; Conservative 0; Mismatches 212; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .3443
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 3443)
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Direct Submission
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Best Local S
Matches 401
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1. (bases 1 to 760)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Score 259.2; DB 12; Length 1079;
Pred. No. 3e-54;
0; Mismatches 243; Indels 5;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Matches 430; Conservative
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/organism="Homo sapiens"

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cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2856 row, o column: 07 Plate: LLCM2856 row, o column: 07 High quality sequence stop: 643.
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I (bases 1 to 754)

NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Produrement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Conscrtium/LLNL at:

Plate: LLAM12030 row: G column: 13

High quality sequence stop: 729.
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27.2%; Score 253.6; DB 12; Length 754;
Best Local Similarity 67.2%; Pred. No. 6.6e-53;
Matches 357; Conservative 0; Mismatches 174; Indels 0;
     669 GCACAATATTGATGTGTTTTCTCGAGATGTGTATGGAAAGC 709
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Search completed: April 30, 2004, 13:07:36 Job time : 2529 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nu	nucleic search, using sw model
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Title: Perfect score: Sequence:	US-10-079-137B-343 933 1 atggtggttgaggttgattctgtttctagtcatcatcatg 933
Scoring table:	OLIGO NUC Gapop_60.0 , Gapext 60.0
Searched:	3470272 segs, 21671516995 residues
Word size :	0
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing: Listing	; Listing first 45 summaries
Database :	1: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		ο̈́o	ARZ/8350 Sequence AR367286 Seguence	AR400322 Sequence	AR405589 Sequence	AR433323 Sequence	AX141041 Sequence	AX267557 Sequence	AX316977 Sequence	AR261058 Sequence	ARZ78589 Sequence	AR400321 Sequence	AR405588 Sequence	AR433322 Sequence	AXI41040 Sequence	AX267556 Sequence	AX282954 Sequence	AR148112 Sequence	BD242264 Compounds	AR260940 Sequence	AR350934 Sequence	AR350935 Sequence	AR367167 Sequence	AR371063 Sequence AR400203 Semience	AR405470 Sequence	AR43310 Sequence	AK43311 Sequence		AX200736 Sequence			AX31695# Sequence	Composit		Compound	AKZ60944 Sequence) 				linear PAT 29-JAN-2003		124					engine mounted in vehicle	
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Unclassified.

I (bases 1 to 879)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,

Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,

Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,

Hepler, W.T. and Henderson, R.A.

Compositions and methods for the therapy and diagnosis of procancer

Location/Qualifiers

Location/Qualifiers

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Lases 1 to 879)

Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Sequence 531 from patent US 6620922.
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                                                                                                                                                                                                                                       (bases 1 to 879)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and
Day, C.H.

Compositions and methods for therapy and diagnosis of prostate
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     TICTCAAGATCTGGAAAGACGCCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
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Location/Qualifiers
1. .879
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Pred. No. 0;
0; Mismatches
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/mol_type="genomic DNA"
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Sequence 531 from patent
AR367286
AR367286.1 GI:34600261
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larity 99.8%;
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                                                                                     342 AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT
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Location/Qualifiers
1. 879
/organism="unknown"
/mol_type="genomic DNA"
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Sequence 314 from patent US 6656480.
AR433323.1 GI:40196105
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches
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Unclassified.
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1 (bases 1 to 879)
2 (bases 1 to 879)
2 (bases 2 to 870)
3 (bases 2 to 870)
4 (bases 2 to 870)
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                          GGCCGTACAATGCCAGGAAGATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC
                                                                 579 AAATAITCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA
                                                                                         522 AATATICCAGAIGAGTAIGGAAATACCACTCTACACTATGACTGTCTACAATGAAGAAAA
                                                                                                                                                819 IGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
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78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels
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Location/Qualifiers
l. 879
/crganism="unknown"
/mol_type="genomic DNA"
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Sequence 531 from patent US 6630305.
AR405589
AR405589.1 GI:40154426
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Retter,M.W. and Dillon,D.C.
Compositions and methods for the treatment and diagnosis of breast 99 CAGGGGGAGCGCCAAGAGGAACGTGGGCACTTCTGGAGACCACACAACGACTCCTCTGTGAA Gaps ö 6; Length 879; 2; Indels linear

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                   ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAACAAGCATGG
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 <u> CGGCAAGAGCAACGTGGGCGCTTGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG</u>
                                                                                                          CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                                                                                                                                                                                                                  Compositions and methods for the therapy and diagnosis of prostate
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CORIXA CORPOSATION (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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                                 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Beed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J. compositions and methods for the therapy and diagnosis of I
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mashiki, Z. and Harada, J.
Negative pressure control apparatus for engine mounted in vehicle
Patent: US 6321716-A 530 27-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 762 IGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTACT
GCTGGACAGACGATGTCCAACTTAATGTCCTTGACAAAAAGAGGACAGCTCTGACAAA
                                                GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC
                                                                 GGCCGTACAATGCCAGGAAGATGAATGTGCTTAATGTTGCTGGAACATGGCACTGATCC
                                                                                                            AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA
                                                                                                                                                                        ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAACAAGCATGG
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al Similarity 99.8%; Pred. No. 0;
833; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C., Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H. Compositions and methods for the therapy and diagnosis of breast
                                                            642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTTAAT
                                                                                                            CAAGAAAAAGGGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC
                                                                                                                                                        TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
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                                                                                             CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC
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CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            Sequence 314 from Patent WO0190152. AX316977

    .879
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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(bases 1 to 1852)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and Day,C.H.
Compositions and methods for therapy and diagnosis of prostate
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/organiam="unknown"
/mol_type="genomic DNA"
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1 (bases 1 to 1852)
Xu,J. Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of pi
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/organism="unknown"
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Length 1852,
                                      2; Indels
    DB 6;
Score 733; DB Fred. No. 0; O; Mismatches
  Query Match
Best Local Similarity 99.8%;
Matches 833; Conservative
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PAT 18-DEC-2003

linear

1852 bp D from patent US 6620922.

Sequence 530 AR400321 AR400321.1 AR400321

RESULT 14 AR400321 LOCUS

GI:40143584

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Unclassified.

Unclassified.

(bases 1 to 1852)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Patent: US 6630305-A 530 07-OCT-2003;
Location/Qualifiers
1. 1852
/organism="unknown"
/mol_type="genomic DNA"
                                  AR405588
Sequence 530 from patent US 6630305.
AR405588
AR405588.1 GI:40154425
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759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818	31 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 1490	819 IGIAIGIIGGGAICAGCAAGTAIAGICAGCCCTCTACTIGAGCAAAAIGTIGAIGTAIC 878	1491 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTAGTATC 1550	879 ITCTCAAGAICTGGAAAGACGGCCAGAGAGTAIGCIGITICIAGICAICAICAIG 933	1551 TICTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 1605
759	1431	819	1491	879	1551
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Search completed: April 30, 2004, 15:23:55 Job time : 3749 secs

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The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for biological sample the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 343; 308pp; English
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                                                             April 30, 2004, 13:07:43; Search time 426 Seconds (without alignments) 9304.152 Million cell updates/sec
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version 5.1.6
- 2004 Compugen Ltd.
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                                           OM nucleic - nucleic search, using sw model
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54	Adall392 Human bre	Adc15365 Human bre	0	~		Aaa06591 Human imm	Aac81004 Human B11	Aac81003 Human bre	Aah93707 Human pro	Aai67209 B305D iso	Aas63800 Human pro	Aah02772 Prostate	Aah85021 Human pro		Ab195171 Human B30	Aas99850 Breast tu	Aas99849 Breast tu	Abk46893 Human bre	Abk46894 Human bre	Acc95335 Prostate	Adall371 Human bre
ACC95453	ADA11392	ADC15365	ADB13980	AAV68992	AAV68993	AAA06591	AAC81004	AAC81003	AAH93707	AA167209	AAS63800	AAH02772	AAH85021	ACA59608	ABL95171	AAS99850	AAS99849	ABK46893	ABK46894	ACC95335	ADA11371
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ALIGNMENTS

Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; New polymucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer. Persing DH; Houghton RL, tumour protein DNA, SEQ ID 343. Foy TM, Dillon DC, ADC15395 standard; DNA; 933 BP 07-AUG-2001; 2001US-00924400. 20-FEB-2002; 2002US-00079137. 02-AUG-2002; 2002US-00212679. 05-AUG-2002; 2002WO-US024917 (first entry) Fanger GR, Hirst SK,

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100.0%; Score 933; DB 9; Length 933;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 933; Conservative 0; Mismatches 0; Indels
                                      Sequence 933 BP; 272 A; 201 C; 248 G; 212 T; 0 U; 0 Other;
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The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample win amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predecermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proceins and nucleic acids, which simulates and/or expands I cells specific for the tumour protein. The present sequence was used to
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                                                                                                                                                           Human breast tumour protein DNA,
ВР.
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20-FEB-2002; 2002US-00079137.
02-AUG-2002; 2002US-00212679.
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ADC15394 standard; DNA; 876
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20-FEB-2002; 2002US-00079137.
02-AUG-2002; 2002US-00212679.
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Local Similarity 99.8%;
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28-OCT-1999; 99US-00429755.
23-MAR-2000; 2000US-00534825.
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Dillon DC;

Retter MW,

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The present sequence is given in a specification relating to compositions and methods for the treatment and diagnosis of breast cancer. Nucleotide sequences that are preferentially expressed in breast tumour lissue, and the polypeptides encoded by such nucleotide sequences, are used in compositions and vaccines to inhibit the development of cancer, especially breast cancer. The progression of a cancer may be monitored by points and comparing the results from the different time points. On and/or CDS+ T-Cells isolated from the cancer patient may be treated with tumour-specific polypeptides, polypurcleotides encoding the polypeptides or antigen presenting cells expressing the polypeptides or antigen presenting cells expressing the polypeptides. The cells are then administered to the patient to inhibit development of cancer
                                                                                                                                                                             An isolated polypeptide comprising an immunogenic portion of a breast tumor protein used for inhibiting the development of cancer, especially breast cancer, and monitoring cancer progression in a patient.
                                                                    Misher LE,
                                                                                                                                                                                                                                                                       Claim 4; Page 185-186; 187pp; English
                                                                    Reed SG,
                                                                 Smith JM,
                                                                                                             WPI; 2000-628403/60.
P-PSDB; AAB28636.
                   (CORI-) CORIXA CORP.
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Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

218 CAGGGGGGGCGCCAAGAGGAACGTGGGCCTTCTGGAGACCACAACGACTCCTCTGTGAA 101 161 278 221 338 281 398 341 458 401 518 461 578 521 638 581 698 641 CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA CGGCAAGAGCAACGTGGGCGCTTGGGGAACTACGATGACAGCGCCTTCATGGATCCCAG cedcaagaccaacerecerressaacraceareacaccaccerreareareceae CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACGGATGTGAACAAGAGGGACAAGCA GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGATCC **AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA** ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAAACAAGCATGG GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT GTACCACGTCCATGGAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGTGATGTGAACAAGAGGGACAAGCA AAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT AAAGAGGACTGCTCTGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAAGAGGACAGCTCTGACAAA GCTGGACAGACGATGTCATTAATGTCCTTGACAACAAAAAGAGACAGCTCTGACAAA GGCCGTACAATGCCAGGAAGATGAGATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA Gapa ö Score 733; DB 3; Length 879; Pred. No. 0; 0; Mismatches 2; Indels tch 78.6%; al Similarity 99.8%; 833; Conservative 579 Query Match Best Local S 66 42 159 102 162 282 399 342 402 462 522 219 279 222 339 519 639 Matches ठ 셤 ò Dp ò g 셤 g ò 셤 셤 g ð δ ò ò g ò

761 878 821 701 Human prostate-specific cDNA sequence splice variant open reading frame. TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC CAAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAAATTTTTAAT 642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGAAATTTTTAAT TTCTCAAGATCTGGAAAGACGCCCAGAGAGTATGCTGTTTCTAGTCATCATG 933 TTCTCAAGATCTGGAAAGACGGCCAGAGAGAGTATGCTGTTTTTAGTCATCATCATG Human, prostate cancer, prostate-specific, diagnosis, vaccine, cytostatic, gene therapy, metastasis, ss. BP. 16-JAN-2001; 2001WO-US001574. AAH93826 standard; cDNA; 879 14-JAN-2000; 2000US-00483672. Dillon DC, Mi MD, Fanger GR, Ku J, Dillon DC, M: Kalos MD, Fanger GR, Wang A, Meagher MJ; (first (CORI-) CORIXA CORP. WO200151633-A2 Homo sapiens 19-JUL-2001 762 669 759 702 819 879 AAH93826 AAH93826 g ઠે g ò ò 셤

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and cancer that a also used in the detection of cancer in a patient. (I) and cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate or ancer. They can indicate the level of metastasis as well as the prostate volume. AAH93137 to AAH9314 and AAM01115 to AAM01318 represent the present

diagnosing, use in

for

New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and

WPI; 2001-425873/45.

Claim 1; Page 408; 543pp; English.

vaccines

Y, Reed SG; Skeiky YAW

SL, Jiang) Stolk JA,

Harlocker S Retter MW,

Mitcham JL, GR, Day CH,

Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

DB 4; Length 879 Score 733; I Pred. No. 0; 78.6%; 99.8%; Query Match Best Local Similarity

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New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 408; 579pp; English.
                                                                                                                                           09-MAY-2000; 2000US-0056B100;
12-MAY-2000; 2000US-0056B100;
13-UNA-2000; 2000US-0059793;
27-UNA-2000; 2000US-006978315;
09-AUG-2000; 2000US-00638215;
29-AUG-2000; 2000US-00657279;
02-OCT-2000; 2000US-00678166;
09-NOV-2000; 2000US-00681166;
                                                                                     27-MAR-2001; 2001WO-US009919
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  WO200173032-A2
                                             04-OCT-2001
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Kalos MD; Carter D;

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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The prostate specific polynucleotide of the invention
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aplice variant #11 open reading

clone B305D

CDNA

(first entry)

29-JAN-2002

AAS63919;

Human; prostate cancer; ss; cytostatic; immunostimulant; tumour

sapiens

Homo

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833; Conservative
                                                                                                                                  Local Similarity
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diagnosis and therapy o
                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.
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Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                            Human prostate-specific sequence related cDNA sequence.
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, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide comprising at least prostate-specific protein, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Page 308; 325pp; English
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Kalos MD, Retter MW, Stolk JA,
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99US-00443686
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18-NOV-1999;
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The present invention describes an isolated polypeptide (PI) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymucleotides (NI) encoding (PI). (PI) and (NI) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic actids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate appecific antigen (PSA) P501S was located on chromosome 1.

AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
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                                                                                                       Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA; gene; ss.
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Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate specific protein and its encoding polynucleotide, useful treatment and diagnosis of prostate cancer.
TICTCAAGAICTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           on DC, Mitcham JL, Harlocker SL, Jiang Y, Retter MW, Stolk JA, Day CH, Vedvick TS, 3 A, Skeiky YAW, Hepler WT, Henderson RA, Houghton RL, Y De BassolsCV, Foy TM;
                                                                                          Prostate cancer therapy associated cDNA #464
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04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
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MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
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Mcneill PD, Houghton RL,
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presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20020192763
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                                                                                                             Score 733; DB 5; Length 879;
Pred. No. 0;
0; Mismatches 2; Indels
                                                                                    Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
                                                                                                             78.6%;
                                                                                                             Query Match
Best Local Similarity 99.8
Matches 833; Conservative
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ABL95290 standard; cDNA; 879

The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the

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42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACCACGACTCCTCTGTGAA 101
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                                                     DB 6; Length 879;
                           Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
                                                                           2; Indels
                                                  Score 733; DB 6
Pred. No. 0;
0; Mismatches
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                                                  Query Match 78.6%;
Best Local Similarity 99.8%;
Matches 833; Conservative
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   described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA
                                                                       Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                               Human B305D cDNA sequence SEQ ID NO 531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 531; 87pp; English.
                                                                                                                                                                                                                        01-AUG-1997; 97US-00904804.
25-FEB-1998; 98US-00020956.
26-FEB-1998; 98US-00015057.
14-JUL-1998; 98US-00115453.
15-JAN-1999; 99US-00115453.
15-JAN-1999; 99US-00132149.
09-APR-1999; 99US-00232149.
12-NOV-1999; 99US-00483672.
14-JAN-2000; 2000US-00483672.
14-JAN-2000; 2000US-00588100.
12-MAY-2000; 2000US-00588100.
12-MAY-2000; 2000US-00588100.
12-MAY-2000; 2000US-0058113.
13-JUN-2000; 2000US-0058113.
13-JUN-2000; 2000US-0058113.
13-JUN-2000; 2000US-0058113.
13-JUN-2000; 2000US-0058113.
13-JUN-2000; 2000US-0058113.
10-AUG-2000; 2000US-00585113.
27-AUG-2000; 2000US-00585113.
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                       (first entry)
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WANG A...
SKEIKY Y A W...
HEPLER W T...
HENDERSON R A...
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MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
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                                                                                                            Homo sapiens
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ABL95290;
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New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer in a patient.
                                                                GCTGGACAGACGATGTCAACTTAATGTCCTTGACAAAAAAGAGGGACAGCTCTGACAAA
                                                                                                                                                                                                                                                                                     AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel breast tumour polynucleotides and polypeptides. The polypeptides and polynucleotides are useful in pharmaceutical compositions for treating and/or preventing cancer, particularly breast cancer, and for eliciting an immune response, particularly humoral and/or cellular immune response. The polynucleotides may be used as probes or primers for nucleic acid hybridisation, in the design and preparation of riboxyme molecules for inhibiting expression of tumour polypeptides and proteins, and in recombinant DNA molecules to direct expression of a polypeptide in host cells. AAS99570-AAS99888 represent novel human breast cancer protein coding sequences and PCR primers of the invention
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                                                      Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 879;
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Skeiky YAW, Harlocker SL, Day CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 733; DB
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000; 2000US-00577505.
08-UTN-2000; 2000US-00590583.
26-CTN-2000; 2000US-0069295.
16-MAR-2001; 2001US-00810936.
                                                                                                                                                                                                                                                                                                                                            22-MAY-2001; 2001WO-US016776.
                                                                                           tumour; vaccine; immunogenic
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Best Local Similarity 99.8%;
Matches 833; Conservative
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ADAl1393 standard; cDNA; 879

(first entry)

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RESULT 13
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                                        The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
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                                                                                                                                               Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
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              Example 11; Page 475; 691pp; English
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Best Local Similarity 99.8
Matches 833; Conservative
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The invention relates to a breast tumour polynucleotide selected from one of the 275 fully defined nucleotide sequences (a) given in the specification, including their complements, sequences consisting of at least 20 contiguous residues of a sequence in (a), sequences that sequences having at least 75 or 96 identity to a sequence in (a), or degenerate variants of a sequence in (a). Also included are an isolated belynpeptide (II) (comprising an amino acid sequence selected from polypeptide (II) (comprising an amino acid sequence selected from sequences encoded by (a), sequences having at least 70% or 90% identity to a sequence in (c), and sequences of 30 fully defined amino acid sequences (c), and sequences having at least 70% or 90% identity to a sequence in (c)), expression vectors comprising (a), a host cell transformed or transfected with the expression vector, an isolated antibody or its antigen-binding fragment that specifically binds to (II),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New breast tumor proteins nucleic acids encoding such proteins, useful diagnosing, preventing and/or treating diseases such as cancer, particularly breast cancer, and as markers for detecting the presence or
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                                                                                                    ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
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                                                                         Human breast cancer specific full length cDNA B305D-A ORF
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, Day CH,
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Harlocker SL,
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                                                                                                                                                                                                                                  11-JAN-1996; 96US-00585392.
10-JAN-1997; 97WG-US000485.
09-APR-1997; 97US-00931782.
17-APR-1999; 99US-00281198.
23-MAR-2000; 2000US-00534825.
24-MAY-2000; 2000US-00577505.
09-JUN-2000; 2000US-00577505.
26-OCT-2000; 2000US-0059753.
26-OCT-2000; 2000US-0059753.
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SMITH J M.
MISHER L E.
DILLON D C.
RETTER M W.
WANG A.
SKRIYY A W.
HARLOCKER S L.
DAY C H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TN, Reed SC
Skeiky YAW,
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P-PSDB; ADA11394.
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Wang A, Skei
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(REED/)
(SMIT/)
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(MISH/)
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(WANG/)
(SKEI/)
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(DAYC/)
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us-10-079-137b-343.olig.rng

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protein comprising the presence of a cancer in a patient, a fusion protein comprising at least one polypeptide (II), an oligomucleotide that hybridises to (a), under moderately stringent conditions, a method for stimulating and/or expanding T cells specific for a tumour protein (by contacting T cells with at least one component selected from (by antigen-presenting cells that express (II), an isolated T cell population comprising T cells prepared from as detailed above, a method for stimulating an immune response or treating cancer in a patient by administering a composition comprising (a), (II), the vector, cells or the antibodies, and a method for inhibiting the development of a cancer. The polypoptides may be used in the design and preparation of ribboyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells. The breast tumour proteins are useful as markers to indicate the presence or absence of a cancer, such as breast cancer, and in the detection of other cancers. Compositions comprising the breast tumour proteins are useful in diagnosing, comprising and/or treating diseases such as cancer, particularly breast funcer. The present sequence is a breast cancer, particularly breast funcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
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Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

ö 518 578 638 698 758 818 218 278 221 338 281 398 341 458 401 461 521 581 641 701 761 161 caededededecaecaagaecaacereceaerreregaeaecaeaacaerecrerereaa 101 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGAAG CCTCACACCACTACTAGTATACATGAGCAAAACAGCAAGTGGAGTGAAATTTTTAAT GACGCTTGGGAGCAAGAGGTGCTAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGAAG CGGCAAGAGCAACGTGGGCGCTTGGGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG CGGCAAGAGCAACGTGGTTGCTTTGGGGACACTACGATGACAGCGCCTTCATGGATCCCAG GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAAAGAGACAGCTCTGACAAA AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGADATCGAATCAAAAAACAAGCATGG CCTCACACCACCACTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGGAAATTTTTAAT CAAGAAAAAGGGAATTTAAATGGGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT AAAGAAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAAACTCGT GGCCGTACAATGCCAGGAAGATGAGATGTGCGTTAATGTTGCTGGAACATGGCACTGATCC GTACCACGTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGT Gaps ö DB 7; Length 879; 2; Indels Score 733; DB Pred. No. 0; Mismatches Ouery Match Best Local Similarity 99.8%; Matches 833; Conservative (342 459 519 642 219 222 399 579 66 42 159 102 162 279 339 282 669 759 유 경 원 음 성 유 6 6 6 8 8 8 g g g B B දු පු 8 8 8 ઠે ò Db ò 장염

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The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer; in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands I cells specific for the tumour protein. The present sequence was used to
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819 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
762 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATGTATC
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                                                                 TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG
                                                                                                                                                                                                                                                                                                         Cytostatic; Gene therapy; breast cancer; breast tumour protein;
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels
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20-FEB-2002; 2002US-00079137.
02-AUG-2002; 2002US-00212679.
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                                                                                                                                                                               ADC15366 standard; DNA; 879
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Kalos MD;
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97US-00904804. 98US-00020956. 98US-00115453. 98US-00159812. 99US-00232149. 99US-00352616. 99US-0043686. 99US-0043686.

2000US-00536857. 2000US-00568100. 2000US-00570737. 2000US-00593793.

14-JAN-2000; 2 27-MAR-2000; 2 09-MAY-2000; 2

18-NOV-1999;

12-MAY-2000; 2 13-JUN-2000; 2 27-JUN-2000; 2

29-AUG-2000; 2000US-00605783. 09-AUG-2000; 2000US-006562183. 29-AUG-2000; 2000US-00651236. 06-SEP-2000; 2000US-00657777.

02-OCT-2000; 2000US-00679426. 10-OCT-2000; 2000US-00685166. 09-NOV-2000; 2000US-00709729.

29-JUN-2001; 2001US-00895814

Xu J, Stolk JA, Kalos MD;

(CORI-) CORIXA CORP.

1; 2001US-00852911

12-JAN-200: 09-FEB-200:

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162 cescaasadeaacenesroscrresesasacraceareaceacerrearesareceae
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Human; ss; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; call thistocompatibility complex allele; MHC; prostate cancer;
                                                                         Human prostate specific cDNA B305 splice variant #11 ORF
        ADB13981 standard; cDNA; 879 BP.
                                                                                                                                        tumour, antigen presenting cell
                                                     18-DEC-2003 (first entry)
                                                                                                                                                                                     US2003185830-A1.
                                                                                                                                                              Homo sapiens.
                                ADB13981;
ADB13981
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RESULT 15

97US-00806099

25-FEB-1997;

12-NOV-2002; 2002US-00294025

02-OCT-2003

New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer. WPI; 2003-756193/71. P-PSDB; ADB13982.

Example 11; Page; 101pp; English.

The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB1353 comprising a sequence ADB1487. The fargement ADB13563 comprising a sequence ADB1487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MFC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific contains and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the proteins and peptides, expression vectors, a host cell fragment) that pencifically binds to the protein or polypeptide or a polypeptide that binds to che agent and comparing the amount of polypeptide to a predetermine the presence of cancer, a fusion protein or off value to determine the presence of cancer, a fusion protein or opposition of polypeptide that binds to opecific for a tumour protein comprising contacting T cells of patient comprising the peptides or proteins, stimulation, tracting prostate cancer in a patient and treating prostate cancer in a patient comprising determining the presence of cancer in a patient and treating prostate cancer in a patient comprising cluster of differentiation (CD4+) and/or CD8+ T cells included or composition of the proteins so that the T cells proliferate, and administering the peptides or an ingen presence of cancer in a patient. The peptides or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides or an oligonucleotide or the hybridises to nucleic acid encoding them), is used to see the presence of cancer in a patient. The peptides of an oligonucleotide or expand T cells specific for a tumour protein, the peptides or the peptides or expand T c

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showing sequence similarity to one of the disclosed human prostate specific cDNAs. Note: Except where otherwise indicated, the sequence data for this pater to fine printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
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Patent No. 6329505
Sequence 531, Application US/09439313
Patent No. 6329505
Sequence 532, Jianglan US/09439313
APPLICANT: No. Jianglun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Glang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Ralos, Michael
APPLICANT: Red, Steven G.
APPLICANT: Retter, Mark
APPLICANT: Red, Steven G.
THILE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: Day, Canig
TITLE OF INVENTION: UNMERR: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 531
SEQ ID NO 531
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US-09-598-226-211

US-09-429-136-211

US-09-429-135-211

US-09-429-133-371

US-09-62-451-297

US-09-285-16A-371

US-09-285-16A-371

US-09-429-755-297

US-09-429-755-298
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-636-215-531

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CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACGGATGTGAACAAGAGGGACAAGCA 341
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US-09-636-215-531
Sequence 531, Application US/09636215
Patent No. 662092
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc W.
APPLICANT: Ut, Samuel
APPLICANT: Carter, Jarrick
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Li, Samuel
APPLICANT: Stolk, John A.
APPLICANT: Stolk, Milliam
TITLE OF INVENTION: Dardows S.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFURABNER: FREESEQ for Windows Version 3.0
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LENGTH: 879
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                    102 GACGCTTGGGAAGCAAGAGGTGCTAGCTGCCACTGCTTCCCTGCTGCAGGGGAG
                                                                                                                                                  162 CGGCAAGAGCAAGTGGTCGCTTGGGGAGACTACGATGACAGGGCCTTCATGGATCCCAG
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                                            99 CAGGGGGAGCGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA
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  Length 879;
                       Indels
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   DB 4;
Query Match
78.6%; Score 733; DB
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches
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Sequence 531, Application US/09685166A

FALCH NO. 6630305

GENERAL INFORMATION:
APPLICANT: ALL Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer I.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
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CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA 398
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                                    102 CAGAAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAAGAACTGCTCTCATACTTGC
                                                                                  819 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
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                                                                                                                                                                            Sequence 314, Application US/09429755A

Facent No. 6656480

GREEAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reich, John M.
APPLICANT: Reich, Seven G.
APPLICANT: Reich, Jana M.
APPLICANT: Reter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 314
LENGTH: 879
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Best Local Similarity 99.8%; Pred. No. 0
Matches 833; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-429-755-314
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APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Rater, Marcy R.
APPLICANT: Retter, Marcy R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Oraig H.
APPLICANT: Darrick
APPLICANT: Darrick
APPLICANT: Darrick
APPLICANT: Mang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Hones S.
APPLICANT: Wang, Aljun
APPLICANT: Hones S.
APPLICANT: Hones S.
APPLICANT: Mang, Aljun
APPLICANT: Hones Compositions AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPRENCES: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT PILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE FASELSE for Windows Version 3.0
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches
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CRGANISM: Homo sapiens
US-09-685-166A-531
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AAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA
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# Sequence 530, Application US/09439313

# Patent No. 6329505

# GENERAL INFORMATION:
# APPLICANT: Xu, Jiangchun
# APPLICANT: Dillon, Davin C.
# APPLICANT: Harlocker, Susan Louise
# APPLICANT: Harlocker, Susan Louise
# APPLICANT: Ralos, Michael
# APPLICANT: Red, Stewn G.
# APPLICANT: Rete, Michael
# APPLICANT: Rete, Michael
# APPLICANT: Rete, Michael
# APPLICANT: Rete, Michael
# APPLICANT: Reter, Mark
# APPLICANT: Reter, Mark
# APPLICANT: Reter, July
# APPLICANT: Reter, July
# APPLICANT: Reter, July
# APPLICANT: Solk, John
# APPLICANT: Day, Craig
# APPLICANT: Solk, John
# APPLICANT: Day, Craig
# APPLICANT: Solk, John
# APPLICANT: Day, Craig
# APPLICANT: D
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78.6%; Score 733; DB
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches
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CORGANISM: Homo sapiens
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US-09-636-215-530
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US-19-16-212-215

Batent No. 662092

GENERAL INFORMATION

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Davin C.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Robert A.

APPLICANT: Harlocker, Robert A.

APPLICANT: Harlocker, Robert A.

APPLICANT: Harlocker, Robert A.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Stelker, John A.

APPLICANT: Stelker, Thomas S.

APPLICANT: Carter, Davi Craig H.

APPLICANT: Carter, Darrick

APPLICANT: Skelky, Yssir A. W.

APPLICANT: WIlliam

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: LIANGERS OF PROSTATE CANCER

TITLE OF INVENTION: LIANGERS OF SECURIOR OF SECURATE COMRENT FILING DATE: 2000-08-10

NUMBER OF SECIENCE: 2001-08-10

SOFTWARE FERSERGER FOR WINDOWS VERSION 3.0

SEQ ID NO 530

LENGTH: 1852

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                                                    DB 4; Length 1852,
                                                                           2; Indels
                                                 Score 733; DB ; Pred. No. 0; 0; Mismatches
                                              Query Match
Best Local Similarity 99.8%;
Matches 833; Conservative
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-530
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US-09-685-166A-530
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Sequence 530, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Raios, Michael D.
APPLICANT: Raios, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Scolk, John A.
APPLICANT: Scolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Gare, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Bear, Milliam
TITLE OF INVEWTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVEWTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVEWTION: DIAGNOSIS OF PROSTATE
CURRENT FALING DATE: 2000-10-10
CURRENT FALING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH ARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 833; Conserv
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1431 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 1490
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Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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ZIF: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/991,789A

FILING DATE: 11-Dec-1997

CLASSIFICATION: «UNROWN->
ATTORNEY/AGENT INFORMATION:
NAME: POCLEE, Jane E. R.
REGISTRATION NUMBER: 33.332

REFERENCE/DOCKET NUMBER: 210121,419C3

TELECOMMUNICATION INFORMATION:
THE REPRESENTED TO THE TOWN TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-08-991-789A-291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-991-789A-291/c
; Sequence 291, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 291: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Washington
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CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAAT 1430
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                                                                                       1431 CAAGAAAAAGGGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC
                                                                                                                                                         819 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTAT
                                                                                                                                                                                            1491 IGIALGIAGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGTATC
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Patent No. 6656480

GENERAL INFORMATION:
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Rede, Steven G.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER TITLE OF INVENTION TREATMENT AND DIAGNOSIS OF BREAST CORRENT FILING DATE: 1999-10-28

CURRENT FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 315

SOFTWARE: FARERER FOR FOR WITH AND SOFTWARE: PARERER FOR FOR WITHOUT AND SOFTWARE.
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FastSEQ for Windows Version 3.0
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Best Local Similarity 99.8
Matches 833; Conservative
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TYPE: DNA
ORGANISM: Homo sapien
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US-09-062-451-291/c
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SEQ ID NO 366
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JOS-097-397-397-305/C

JOSEPTEL INFORMATION

JAPPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Harlocker, Jennifer L.

APPLICANT: Harlocker, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Harlocker, Susan Louise

APPLICANT: Kalos, Michael

APPLICANT: Kalos, Michael

APPLICANT: Red, Steven G.

APPLICANT: Red, Steven G.

APPLICANT: Reter, Mark

APPLICANT: Setter, Mark

APPLICANT: Solk, John

APPLICANT: Solk,
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Patent No. 6344550
GENERAL INFORMATION:
PAPPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
  Length 1851;
                                                 1; Indels
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  DB 4;
Query Match 69.2%; Score 646; DB Best Local Similarity 99.9%; Pred. No. 0; Matches 696; Conservative 0; Mismatches
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344 AAGTATAGTCAGCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAAG 285
                                                          897 ACGCCAGAGAGTATGCTGTTTCTAGTCATCATG
                                                                                284 ACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       Sequence 292, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID N. SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.9
Matches 696; Conservative
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US-09-062-451-292
                                                                                                                                                   RESULT 12
US-09-062-451-292/c
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                                                                                COMPUTER: TENDARY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FLING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: MAKA, DATIG J. 392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 310121.419C2
TELEPONMULCATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INPORMATION POR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: MOLOLeic acid
STRANDEDNESS: single
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99.9%; Pred. No. 0;
live 0; Mismatches
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Best Local Similarity 99.9
Matches 696; Conservative
                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-062-451-291
                                  USA
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APPLICANT: SMITH, JOHN M.
APPLICANT: SMITH, JOHN M.
APPLICANT: SMITH, JOHN M.
APPLICANT: SMITH, JOHN M.
APPLICANT: REACH, STEVEN G.
TITLE OF INVENTION: CRMCOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
ADDRESSEE: SEED AND BRERY LLD
STREET: G300 COlumbia Center, 701 Fifth Avenue
CITY: Seatle
STREET: Seatle
STREET: Seatle
STREET: SANDALE
STREET: Machington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMMUTER: IAR PC Compatible
OPERATING SYSTEM: D4-D6-D6S/MS-D0S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: US/09/062,451
FILING DATE: MARCHANTANDAMETON
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99.9%; Pred. No. 0;
ive 0; Mismatches 1; Indels
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284 ACGCCCAGAGAGTATGCTGTTTCTAGTCATCATG 248
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69.2%; Score 646; DB 4
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches
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Patent No. 6586570
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US-09-289-198-291
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                                                                                                TGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAAATTAATGGCCAAAGCACT
                            644 AGATGAATGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATGAGTA
                                                                                                                                                             GCTCTTATACGGTGCTGATATCGAATCAAAAACAAGCATGGCCTCACACCACTGCTACT
                                                                                                                                                                                                           TGGTATACATGAGCAAAAACAGCAAGTGGTGAAATTTTTAATCAAGAAAAAAGCGAATTT
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                                                                                                                                        GCTCTTATACGGTGCTGATATCGAATCAAAAACAAGCATGGCCTCACACCCCCTGCTACT
                                                                         TGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAAATTAATGGCCAAAGCACT
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| Sequence 366, Application US/09352616A
| Sequence 366, Application US/09352616A
| Patent No. 639578
| GENERAL INFORMATION:
| APPLICANT: Dillon, Davin C.
| APPLICANT: Harlocker, Susan Louise
| APPLICANT: Jang, Yuqui
| APPLICANT: W., Jiangchun
| APPLICANT: W., Jiangchun
| TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
| TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
| FILE REFERENCE: 210121-427C8
| CURRENT APPLICATION NUMBER: US/09/352,616A
| CURRENT PRILING DATE: 1999-07-13
| NUMBER OF SEQ ID NOS: 472
| SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches
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CORGANISM: Homo sapien
US-09-352-616A-366
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LENGTH: 1851
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APPLICANT: Frudakis, Tony N.
APPLICANT: ATLA, John M.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITION NUMBER: US 09/062,451
EARLIER FILING DATE: 1999-04-09
EARLIER FILING DATE: 1999-04-09
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-03-10
EARLIER FILING DATE: 1997-03-10
EARLIER FILING DATE: 1997-03-10
EARLIER FILING DATE: 1997-03-10
EARLIER FILING DATE: 1996-08-20
EARLIER FILING DATE: 1996-08-20
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FASTESQ FOR WINDOWS VERSION 3.0
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APPLICANT: Misher, Livida
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TEATMENT AND DIAGNOSIS OF BREAST CANCER
FILE OF INVENTION: TEATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REPERBOCE: 210121.41956
CURRENT APPLICATION NUMBER: US/09/289,198
CURRENT PILLING DATE: 1999-04-10
EARLIER FILLING DATE: 1998-04-17
EARLIER FILLING DATE: 1999-12-11
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILLING DATE: 1997-04-09
EARLIER FILLING DATE: 1997-04-09
EARLIER FILLING DATE: 1997-04-10
EARLIER FILLING DATE: 1997-04-10
EARLIER FILLING DATE: 1997-04-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILLING DATE: 1996-01-01
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Patent No. 6586570
GENERAL INFORMATION:
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Pred. No. 0;
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NUMBER OF SEQ ID NOS: 312
) SOFTARER: FastSEQ for Windows Version 3.0
) SEQ ID NO 292.
LENGTH: 1851
) TYPE: DNA
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Matches 696; Conservative
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AL703938 DKFZp686E
B0672700 RPCIII-14
BE06969 CMI BT039
BG72604 F0262528
AG165908 PAN LEGGI
AG596029 HS 2116 B
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K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-All S',
BM763942
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Xim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Homo sapiens (human)
Homo sapiens
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-4470
Fax: +82-42-866-4470
Email: yongsung@mail.kribb.re.kr
Plate: 25 row: A column: 11
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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VERSION
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                                                     April 30, 2004, 14:03:48; Search time 2520 Seconds (without alignments) 11056.117 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop_60.0 , Gapext 60.0
                                    nucleic search, using
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/ organism="Homo sapiens"

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/ lab_ative |
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BM763453 633 bp mRNA linear EST 04-MAR-2002
K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
mRNA sequence.
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I (bases 1 to 633)
Xim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Xim,M.R., Oh,X.J., Cheong,J.B., Sohn,H.Y., Xim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Visecong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
Email: yongsung@mail:kribb.re.kr
Plate: 16 row: A column: 11
Plate: 16 row: A column: 11
High quality sequence stop: 633.
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                                                                                                                                                                                                                                       21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                   BM763453
BM763453.1 GI:19093068
                                                                                                  Homo sapiens (human)
Homo sapiens
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Pred. No. 2e-83;
0; Mismatches 1;
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High quality sequence start: 99
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Site=1: Sfil (gacdgottogaco); Site=2: Sfil
/note="Organ: prostate; Vector: pDNR-LIB (clontech);
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402004215F1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4248746 5',
mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov

Tissue Procurement: CloNETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Caboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distributions MGC clone distribution information can be http://image.lln.gov
Plate: LLCM167 row: m column: 03
High quality sequence stop: 642.
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TGATCCAAATATTCCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGA 240
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                 GCATGGCCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTGCTGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGA
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                                                                                                                   GCATGGCCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAAATT
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BF676987
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| 1.380 | Agantsm="Homo sapiens" | Agantsm="Homo sapiens" | Agantsm="Homo sapiens" | Agantsm="Raxon:9606" | Ada_refe="taxon:9606" | Ada_refe="taxon:9606" | Ada_refe="taxon:960276" | Ada_refe="taxon:960276" | Ada_refe="taxon:970276" | Ada_refe="taxon:97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE322552 380 bp mRNA linear EST 22-NOV-2000 RC6-BN0276-16#600-011-F12 BN0276 Homo sapiens cDNA, mRNA sequence. BF329652
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1 (bases 1 to 380)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAIDSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-BN0276-
160600-011-F12&t3=2000-06-16&t4=1)
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Laboratory of Cancer Gentics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 IGGIGAAATITITAATCAAGAAAAAGGGAATTIAAATGGGCIGGAITGATAGATATGATAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 CAAAAAACAAGCATGGCCTCACACCCACTGCTACTTGGTGTACATGAGCAAAAAACAGCAAG
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Length 865;
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729 bp mRNA linear EST 18-OCT-2002
AGENCOURT_10425351 NIH_MGC_83 Home sapiens cDNA clone IMAGE:6668956
5', mRNA sequence.
EU930826
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400 bp DNA linear GSS 22-SEP-1998
HS_3122_A1_C07_MR CIT Approved Human Genomic Sperm Library D Homo
   182 TCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGTGCTGGACAGACGACGATGTCAACTTAAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 AGGCCGTACAATGCCAGGAAGATGTGCGTTAATGTTGCTGGAACATGGCACTGATC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 AGGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGATC 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611
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                                                                                                                                    122 GTCCTTGACAACAAAAGAGGACAGCTCTGACAAAGG
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Homo sapiens
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Matches 94;
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Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (Bases I to 607)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B48260 607 bp DNA linear GSS 08-APR-1999 RPCIl1-6X4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6X4, Genomic survey sequence.
                                                                                                                                                                                                                                                 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA 158
                                                                                                                                                                                                                                                                                      282 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAACGACTCCTCTGTGAA 223
                                                                                                                                                                                                                                                                                                                                                                                                                 222 GACGCTTGGGAGCAAGAGGGGGCAAGTGCTGCCCACTGCTTCCCCTGCTGCTGCAGGGGAG 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter of Jong Spieces, plater dead on the contact Pieter dead on the contact between the
tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                     159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGGAG
                                                                                                                                                                                         Gaps
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                                                                                                                       Query Match 17.8%; Score 166; DB 10; Length 380; Best Local Similarity 100.0%; Pred. No. 1.4e-77; Matches 166; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162/ CGSGAAGAGAGCAACGTGGGGCGCTTGGGGAGACTACGATGACAGCGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 CGCCAAGAGCAACGTGGGCGTTGGGGAGACTACGATGACAGCGCC 264
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/db_xref="GDB:7502163"
/db_xref="taxon:9606"
/clone="RPCI-11-6K4"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Mahairas, G.G., Wallace, T.C., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX492731 506-Spp mRNA linear BST 04-SEP-2003 DXFZp781C0523_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone DXFZp781C0523_5', mRNA sequence.
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Bukaryotti.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 505)

1 locker H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

EST (Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.) (Unpublished (2003)

Contact: MIPS

MIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
5-Coli DH108"
                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
sapiens genomic clone Plate=3122 Col=13 Row=E, genomic survey
                                                                                                                                                                                                                                                                            scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-3818
Fax: (207) 616-3618
Fax: (208) 616-3618
Fax: (208) 616-3618
Fax: (208) 616-3618
Fax: (208) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 89; DB 28; Length 400; 100.0%; Pred. No. 4.1e-36; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
|mol_trype="genomic DNA"
|db xref="taxon:9606"
|clone="plate=3122 Col=13 Row=E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578 CAAATATTCCAGATGAGTATGGAAATACC 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 CAATATTCCAGATGAGTATGGAATACC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 400.
Location/Qualifiers
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BX492731.1 GI:32004516
                                                          AQ124119.1 GI:3501285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                              Homo sapiens (human)
Homo sapiens
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Best Local Similarity
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DEFINITION
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VERSION
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SOURCE
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MEDLINE
PUBMED
COMMENT
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AUTHORS
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JOURNAL
COMMENT
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                                                      VERSION
KEYWORDS
SOURCE
                                       ACCESSION
                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                  AUTHORS
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dKz-heidelberg.de;
Braunschweig/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZ0781C0523) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMNY; Email: clone@rzpd.de.

Location/Qualifiers

i. 506
/ Organism="Homo sapiens"
/ Ab_Arsf="Hamba"
/ Ab_Arsf="Hamba"
/ Abote="mRNA"
/ Abote="mRNA"
/ Abote="mRNA"
/ Abote="mRNA"
/ Abote="mRNA"
/ Abote="manal"
/ Clone inh="manal"
/ CDNA-collection"
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B. (Dases I to 894)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CLONA Library Preparation: CLONETECH Laboratories, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov
Plate: LLCM1088 row: e column: 12

High quality sequence stop: 576.

Locatan/Qualifiers
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BF675049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 GAGAAGATCTGGACAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCCCAGAAAGGATC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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7.9%; Score 74; DB 13; Length 50
Best Local Similarity 100.0%; Pred. No. 5e-28;
Matches 74; Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
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1....', organism="Homo sapiens"

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/mol_type="mRNA"
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/lab host="MH108"
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/clone="Indec:572364"
/clone="Indec:57364"
/clone="In
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccgctcggcc); Site_2: Sfil (ggccgctcggcc); A adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC3' C' ATTATAGAGCCGACGCGCAAG-4T(30)BN-3' (Where B = A, C' or G' or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nin.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TobNa Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAM11677 row: g column: 21
High quality sequence stop: 236.
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.6%; Score 71; DB 10; Length 89 Best Local Similarity 100.0%; Pred. No. 2.3e-26; Matches 71; Conservative 0; Mismatches 0; Indels
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BI461255.1 GI:15251911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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SOURCE
ORGANISM
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BI461255/c
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TITLE
JOURNAL
COMMENT
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ORIGIN

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/dev_stage="adult"
/lab_host="mylloB"
/clone_lib="NCI_CGAP_Pr28"
/note="Torgan: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Torgan: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Torgan: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Torgan: prostate; Vector: plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, ll01192-1101959, and 1217928-1220615).
Subtraction by Bento Soaxes and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Produrement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Tissue Produrement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnli.gov/bppt/image/image.html
Insert Length: 543 Std Brror: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers
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                                                                                                                                                                                                                                                              AIG04733 451 bp mRNA linear EST 07-MAR-2000 u1432b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 451)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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HS_5144_B1_G01_T7A RPCI-11 Human Male BAC Library Homo sapiens
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                                                 Gaps
                                                                                                                       63 ATGCCGCTGCCTCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGAAGTGGGCAAGT
                                                                                               22 ATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGT
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Length 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ACTGCTCTCATACTTGCTGTATGTTGTGGATCACCAGTATAGTCAGCC
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Pred. No. 1.4e-14;
0; Mismatches 0;
                         1.9e-19;
ch 6.2%; Score 58; DB 12;
1 Similarity 100.0%; Pred. No. 1.9e-15
58; Conservative 0; Mismatches C
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred
0; M
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Homo sapiens
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                       RNA sequence.
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Best Local Similarity
Matches 49; Conserv
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  Query Match
Best Local
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AQ615477
LOCUS
DEFINITION
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AI804733
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AUTHORS
                                                 Matches
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KEYWORDS
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vencer, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Use Distributed (1997)
Unpublished (1997)
Other GSSs: RPCIII-14712.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Rea: 301 838 0208
Eaxi: 301 838 0208
Exail: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S92 bp DNA linear GSS 20-MAY-1999 RPCI11-14712.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-14712, genomic survey sequence.
                                                                                                                                                         This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ), Email s.wiemann@dkfz-heidelberg.de,
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
This clone (DKEZp686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GRRMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1, Chases 1 to 592] [2hao,S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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SST (Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 43; Conservative 0; Mismatches 0; Indels
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Homo sapiens
                        Wiemann,S.)
Unpublished (2001)
Contact: MIPS
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AQ372700
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-3818
Faxi: (206) 616-3819
Faxi: (206) 616-3819
Faxi: (206) 616-381
Faxi: (206) 616-381
Faxi: (207) 700
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/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
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DKFZp686E1728_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686E1728_5', mRNA sequence.
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 531) Mahalaas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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1 (bases 1 to 544)
Ottenwaelder, B., Cbermaier, B., Mewes, W., Mewes, H.W., Weil, B. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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genomic clone Plate=720 Col=1 Row=N, genomic survey sequence.
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AL703938.1 GI:19687293
                                AQ615477
AQ615477.1 GI:5076753
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Homo sapiens
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                                                                                                                                sapiens (human)
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(Dases 1 to 187)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., Gordan, G. Briones, M.R., Madal,M.A., Bordan, G. Geste,F.F., Brunstein,A., deoliveira,P.F., Mateukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Soares,F. Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Email: asimpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-BT0397-201
Seq primer: puc 18 forward
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High quality sequence stort: 82
High quality sequence story: 141.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
/organism="Homo sapiens"
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                     673 GATATCGAATCAAAAACAAGCATGGCCTCACACCACTG
                                       Query Match
4.2%; Score 39; DB 10;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 39; Conservative 0; Mismatches 0
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Search completed: April 30, 2004, 16:06:11 Job time : 2524 secs

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